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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:41:47 ; Search time 1762.93 Seconds  
(without alignments)  
5800.480 Million cells updates/sec

Title: X94938  
Perfect score: 1636  
Sequence: 1 TTTACTCTTCAGTCAGAGA.....AAAAAAAAAAAAAAAAAAAA 1636

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	100.0	1636	21	US-10-764-138-6
2	775.2	47.4	1744	16	US-10-292-408-25
3	733	44.8	1490	21	US-10-477-687-12
4	730.8	44.7	1143	9	US-09-938-842A-875
5	730.8	44.7	1143	11	US-09-938-842A-875
6	724.6	44.3	2519	18	US-10-424-599-124786
7	709	43.3	1621	16	US-10-292-408-15

8	708.6	43.3	1881	18	US-10-424-599-67987
9	707	43.2	1726	18	US-10-425-114-12807
10	707	43.2	1979	18	US-10-424-599-67990
11	705	43.1	1499	16	US-10-292-408-21
12	705	43.1	1553	18	US-10-424-599-26109
13	694.2	42.4	1922	19	US-10-437-963-29872
14	689.8	42.2	1831	19	US-10-437-963-98579
15	689.2	42.1	1744	18	US-10-424-599-67989
16	685.6	41.9	1779	20	US-10-425-115-22950
17	677.2	41.4	1887	18	US-10-425-114-32993
18	668.4	40.9	1614	18	US-10-425-114-17458
19	668.4	40.9	1703	18	US-10-425-114-13850
20	668.4	40.9	1868	20	US-10-425-115-32308
21	667.2	40.8	1673	9	US-09-854-731-15
22	662.8	40.5	1936	19	US-10-437-963-24168
23	654.6	40.0	1828	20	US-10-425-115-32310
24	653.2	39.9	2103	20	US-10-425-115-22953
25	645	39.4	1698	18	US-10-425-114-35222
26	630.6	38.5	1600	18	US-10-425-114-34808
27	630.6	38.5	1645	18	US-10-425-114-4124
28	629	38.4	1711	18	US-10-425-114-22299
29	629	38.4	1818	20	US-10-425-115-148434
30	624.4	38.2	1808	20	US-10-739-930-4849
31	606	37.0	1672	18	US-10-425-114-32862
32	605.2	37.0	1849	16	US-10-232-408-2
33	601.2	36.7	1564	18	US-10-425-114-3272
34	599.6	36.7	1675	18	US-10-425-114-30667
35	599.6	36.7	2573	20	US-10-425-115-111277
36	598	36.6	1766	18	US-10-425-114-26106
37	598	36.6	1807	19	US-10-767-701-14202
38	587.8	35.9	1230	9	US-09-938-842A-2358
39	587.8	35.9	1230	11	US-09-938-842A-2358
40	585.6	35.8	1817	18	US-10-425-114-8223
41	585.2	35.8	1717	18	US-10-425-114-11972
42	584.6	35.7	1635	18	US-10-425-114-9488
43	584.6	35.7	1867	18	US-10-424-599-81473
44	584.2	35.7	2794	19	US-10-437-963-9996
45	582.2	35.6	2165	19	US-10-437-963-24107

## ALIGNMENTS

### RESULT 1

US-10-764-138-6  
; Sequence 6, Application US/10764138  
; Publication No. US20050081266A1  
; GENERAL INFORMATION:  
; APPLICANT: Sudwestdeutsche Saatzeucht-SWS  
; APPLICANT: Advanta Seeds B.V.  
; TITLE OF INVENTION: Modulation of Storage Organs  
; FILE REFERENCE: 026-1  
; CURRENT APPLICATION NUMBER: US/10/764,138  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US/09/578,194  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; TYPE: DNA  
; LENGTH: 1636  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: mRNA  
; LOCATION: (1)..(1636)  
; OTHER INFORMATION: strain Columbia ecotype  
; OTHER INFORMATION: taxon:3702  
; OTHER INFORMATION: tissue type leaves  
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots  
; PUBLICATION INFORMATION:  
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.  
; TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)  
; TITLE: from Arabidopsis thaliana ( Accession No. X94938, x94939 and X99696) ( PGR97-

= instant  
Cage

:	TITLE:	008)
:	JOURNAL:	Plant Physiol.
:	VOLUME:	113
:	ISSUE:	1
:	PAGES:	306-306
:	DATE:	1997-01-01
:	DATABASE ACCESSION NUMBER:	genbank/X94938
:	DATABASE ENTRY DATE:	1998-02-13
:	RELEVANT RESIDUES:	(1)..(1636)
US-10-764-138-6		

  

	Query Match	100.0%	Score 1636;	DB 21;	Length 1636;
	Best Local Similarity	100.0%;	Pred. No. 7.4e-311;	Mismatches 0;	Indels 0; Gaps 0
	Matches 1636;	Conservative			
Qy	1	TTTTACTCTTTCAGTGAGAGAGAAGTTAGAGCTGTAAAGACACATGACTTCGATACCAT	60		
Db	1	TTTTACTCTTTCAGTGAGAGAGAAGTTAGAGCTGTAAAGACACATGACTTCGATACCAT	60		
Qy	61	TGGGGCCTCTCCAGCGCTCCGTCCTTAGTCTCCTCAGCCGCCGATCTTCACGGCGGAGATT	120		
Db	61	TGGGGCCTCTCCAGCGCTCCGTCCTTAGTCTCCTCAGCCGCCGATCTTCACGGCGGAGATT	120		
Qy	121	CTTTGAACAAGTCGTCCCAGATATAGACAACGACAGGAATAAATGTCCTGCTGCTGTTATAGAAG	180		
Db	121	CTTTGAACAAGTCGTCCCAGATATAGACAACGACAGGAATAAATGTCCTGCTGCTGTTATAGAAG	180		
Qy	181	GAAATGATGCTGTACCGGTACACATAATTTCTACTACAATTTGGAGGCCAAAATGCTGAAC	240		
Db	181	GAAATGATGCTGTACCGGTACACATAATTTCTACTACAATTTGGAGGCCAAAATGCTGAAC	240		
Qy	241	CTAAACAGACCAATTAGTTTACATGGCCGAACGTTGTTTGGAAACAGGATCATTCGGAAATTG	300		
Db	241	CTAAACAGACCAATTAGTTTACATGGCCGAACGTTGTTTGGAAACAGGATCATTCGGAAATTG	300		
Qy	301	TATTCCAGGC AAAATGCTTTGAAAACTGGAGAAATCAGTAGCCCAATTAAGAAGGTTTTCGAAG	360		
Db	301	TATTCCAGGC AAAATGCTTTGAAAACTGGAGAAATCAGTAGCCCAATTAAGAAGGTTTTCGAAG	360		
Qy	361	ATCCGCGTTATAA AACCGAGTGGCAATTAATCGGCAATAGTACCAATGC AAATGTGG	420		
Db	361	ATCCGCGTTATAA AACCGAGTGGCAATTAATCGGCAATAGTACCAATGC AAATGTGG	420		
Qy	421	TTTCCTTGAAGCATTTGTTTCTCTCAAACGACTAGAGATGAGCTCTTCCTCAATCTCG	480		
Db	421	TTTCCTTGAAGCATTTGTTTCTCTCAAACGACTAGAGATGAGCTCTTCCTCAATCTCG	480		
Qy	481	TTATGGAGTATGTAC CAGAGACATTTGTACCGGGTTTGAAGCACTATACTAGTTC A AACC	540		
Db	481	TTATGGAGTATGTAC CAGAGACATTTGTACCGGGTTTGAAGCACTATACTAGTTC A AACC	540		
Qy	541	AGCGGATGCCATCTTCTATGTCAAAC TTACACATACCAATCTTTCAGAGCTTTGGCTT	600		
Db	541	AGCGGATGCCATCTTCTATGTCAAAC TTACACATACCAATCTTTCAGAGCTTTGGCTT	600		
Qy	601	ATATCCATAC TGCCTCGTGTCGCCAGAGATATAAAACCA CAAAATCTTTTGGTTG	660		
Db	601	ATATCCATAC TGCCTCGTGTCGCCAGAGATATAAAACCA CAAAATCTTTTGGTTG	660		
Qy	661	ATCCCCACACCCATCAGTGTGAAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGGTGAAG	720		
Db	661	ATCCCCACACCCATCAGTGTGAAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGGTGAAG	720		
Qy	721	GTGAACCAAACATATCATATATCTGCTCTCGGTATTACCGAGCTCAGAACTCATCTTTTG	780		
Db	721	GTGAACCAAACATATCATATATCTGCTCTCGGTATTACCGAGCTCAGAACTCATCTTTTG	780		
Qy	781	GTGCCACAGATATACATCATCATTGTATATATGTTCTGCTGTTGTTCTGGCAGAGC	840		
Db	781	GTGCCACAGATATACATCATCATTGTATATATGTTCTGCTGTTGTTCTGGCAGAGC	840		
Qy	841	TACTTCTTTGGGCAGCCGTTATTTCCGGGAGAAAATTTCTGTGAC CAGCTAGTGGAGATCA	900		

RESULT 2  
 US-10-292-408-25  
 ; Sequence 25, Application US/10292408  
 ; Publication No. US20030182692A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN THIELEN, NOCHA  
 ; APPLICANT: DA COSTA E SILVA, OSWALDO  
 ; APPLICANT: CHEN, RUOYING  
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS  
 ; TITLE OF INVENTION: OF USE IN PLANTS  
 ; FILE REFERENCE: 16313-0178  
 ; CURRENT APPLICATION NUMBER: US/10/292,408  
 ; CURRENT FILING DATE: 2002-11-12  
 ; PRIOR APPLICATION NUMBER: 60/346,096  
 ; PRIOR FILING DATE: 2001-11-09  
 ; NUMBER OF SEQ ID NOS: 51  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 25

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; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-25

Query Match      47.4%; Score 775.2; DB 16; Length 1744;
Best Local Similarity 79.4%; Pred. No. 4.9e-142; Mismatches 238; Indels 0; Gaps 0;
Matches 918; Conservative 0;

QY 129 CCGTCCCGATATAGACACGACAGGAATGTCTGCTGCTGTTATAGAGGAATGAT 188
DB 148 CGGAGCTCCGATGTGGAGACGATAGGATATGTGAGTCTACTGTCTATTGAGGGATGAT 207
QY 189 GCTGTTACGGTCAATATTTCTACTACAATTTGAGGCAAAAATGGTGAACCTTAAACAG 248
DB 208 GCTGTCACTGGCCACATATCTCCACCAATTTGGAGGCAAAAATGGGGAACCTTAAAGAG 267
QY 249 ACCATTAGTTACATGGCGGACGCTGTTGTTGAAACAGGATCATTCGGAATTTGATTCAG 308
DB 268 ACCATCAGTTATACATGGCAGACGCTGTTGTTGCACTGGATCATTTGGAGTTGTTTTTTCAG 327
QY 309 GCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAAGTTTTCGAAGATCGCGGT 368
DB 328 GCAAGTCTTGGAGACTGGAGACGATGGCTATTAAAGGTCTTTCGAAGACAGGCGG 387
QY 369 TATAAAACCGAGAGTTGCAATTAATGACCTAATGAGACCATPCCAAATGTGTTTCCCTTG 428
DB 388 TACAAAAATCGTGAATTCGAGTTAATGGCTTAATGGATCACCCCTAATGTAAATTTCCCTG 447
QY 429 AAGCAATGTTCTTCTCTACACGACTAGATGAGCTTCTTCTCAATCTGTTATGAG 488
DB 448 AAGCACTGTTCTTCTCACACCAAGCAGAGATGAATTTTCTAAATCTGGTAAATGAA 507
QY 489 TATGTACAGAGACATTTGACGGGTTTGAAGCACTATAGTTTCAACACAGCGGATG 548
DB 508 TATGTTCCGGAATCAATGACCGAGTTATAAGCACTACACTACTATGAACAGAGATG 567
QY 549 CCTATCTTCTATGTCAAACTTTTACACATCAACCAATCTTCAGAGGCTTGGCTTATATCAT 608
DB 568 CTTCTCATCTATGTGAACACTGTATACATATCAATCAATCTTTAGGGATTAAGCATATATCAT 627
QY 609 ACTGCTCTGCTGCTGCTCCACAGAGATATAAACCACAAATCTTTGGTTGATCCCCAC 668
DB 628 ACCGCACTGGGAGTTTGCATAGGATGTGAAGCTCAAAATCTTTTGGTTCATCCTCTT 687
QY 669 ACCATCAGTGTAGCTCTGTGATTTTGAAGTGCAAAAGTACTGGTGAAAGGTTGAACCA 728
DB 688 ACTCACAAGTTAAGCTATGTATGATTTTGGAGTGCAAGTTCTGCTCAAGGTTGAATCA 747
QY 729 AACATATCATATATCTGCTCGSPATTTACCGAGCTCCAGAACTCATCTTTTGGTGCCACA 788
DB 748 AACATTTTCATACATATGTTTCAAGTTACTATCGGGCTCCAGAACTAATATTTGGTGCAACA 807
QY 789 GAGTATACATCATCAATGATATATGTTGCTGCTGCTGTTGTTGCGCAGAGCTACTTCTT 848
DB 808 GAATACACAGCTTCTATGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
QY 849 GGGCAGCGGTTATTCGCGGAGAAATTTCTGTGGACACAGCTAGTGGAGATCATAAAGGTT 908
DB 868 GGAAGCCATATTTTCTTGGAGAAACCAAGTGGACCAACTTGTGGAAATTTATCAAGGTT 927
QY 909 CTTGGTACTCCAACCTCGCGAAGAAATCCGGTGATGAACCCAACTACACAGACTTTCAGA 968
DB 928 CTTGGTACTCCAACACGCGAGGAAATCCGTTGTATGAACCCAAATATATACAGAGTTTGA 987
QY 969 TTCCACAAATCAAGGCCACCTTGGCATTAAGGTTTTCACAGCGGATGCTCCGGA 1028
DB 988 TTCCCTCAGATTAAGCTCATCTTGGCACAAGGTTTTCACAGCGGAAATGCTCCCTGAA 1047
QY 1029 GCCATTGACCTTGCATCTCGGCTTCTTCAATCTCACCAAGTCTACGTTGCACTGCGCTC 1088
DB 1048 GCAATTGACCTTGCATCAAGGCTTCTCCAAATATTCACCTAGTCTCCGCTGCACTGCGCTG 1107
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1089 GAGGATGTGGCATCCGTTTTCATGAATCCCTGAGCCAAATGCTGCTTCTTCAAT 1148
1108 GAAGCATGTGCACATCTCTTTCTTGTAGAGCTTCGGAACCAATGCGCGGCTACCTAAT 1167
1149 GCGCGACCTCTACCAACCGTGTTCACATTTCAAAACAGAGTTGTCTGGGGCTTCACCGGAG 1208
1168 GCGCGTCCACTGCGCCCACTTTTCACTTCAACAGAGTTAGCTGGAGCATCACTGAA 1227
1209 CTTATCAACAGGCTAATACCAAGCATGTGAGGCGACAGATGAATGGTGGCTTTCCATTT 1268
1228 CTGATCAATAGGCTCATCCAGAGCATATTAGGCGGCAGATGGGTCTCAGCTTCCGCGCAT 1287
1269 CAAGCTGACCCCTAGA 1284
1288 TCTGCGGTACATAGA 1303

RESULT 3
US-10-477-687-12
; Sequence 12, Application US/10477687
; Publication No. US20050049397A1
; GENERAL INFORMATION:
; APPLICANT: Choe, Sunghwa
; APPLICANT: Feldmann, Kenneth A.
; APPLICANT: Tax, Frans
; TITLE OF INVENTION: DWF12 and Mutants Thereof
; FILE REFERENCE: 11696-075US1
; CURRENT APPLICATION NUMBER: US/10/477,687
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US02/15563
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,342
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: RastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A DWF12 cdna
US-10-477-687-12

Query Match      44.8%; Score 733; DB 21; Length 1490;
Best Local Similarity 77.4%; Pred. No. 8.6e-134;
Matches 889; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 137 CGATATAGACACACACAGGAATGTCTGCTGCTGTTATAGAGGAATGATGCTGTAC 196
DB 196 CGCATGCTGATGATAAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
QY 197 CGGTCAACATAATTTCTACTACAATTTGGAGGCAAAAATGCTGAACCTTAACAGACCATTAG 256
DB 256 TGGTCATATATTTTCCACCAATCGGTGGCAAAAATGCTGAACCAAAAACAGACCAATTAG 315
QY 257 TTACATGCGCCGAACGTTGTTTGGAAACAGGATCAATTCGGAATTTGTTTCCAGGCAAAATG 316
DB 316 TTACATGCGCGAGCGAGTTGTTGTTGACAGCTCGTTCCGGATCGTTTTCAGAGCAAAATG 375
QY 317 CTTGGAACCTGGAGAAATCAGTAGCCATTAAGAAGTTTTCGAAGATCCCGCTTATAAAA 376
DB 376 TTTGGAGACTGGAGAAACCGTGGCGGATAAAGAAGTTTTCGAAGATAGAAGATACAAGAA 435
QY 377 CCGAGAGTTGCAATTAATGCGCACTAATGGACCATTCGAATGTTGTTTCTTGAACATTTG 436
DB 436 CCGAGAACTTCAGTTGATGCGGTGATGGATCATCCGAATGTTGTTTCTTGAACATTTG 495
QY 437 TTTCTTCTCTACAAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATATGTACC 496
DB 496 CTTCTTTTCGACTACAAGTAAGACGAGCTTTTCTTGAATTTGTTATGGAGATATGTCCC 555
QY 497 AGAGACATTTGACCGGTTTGAAGCACTATATAGTTTCAACCAAGCGGATGCCTATCTT 556
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Db 556 TGAGAGCTGTATCGAGTTCTGAAACATATATAGTAGTGCAAAACCAAGAAATGCCTCTGT 615  
Qy 557 CTATGTCRAACTTTACACATACCAATCTTCAGAGCTTGGCTTATATCATCTACTGCTCC 616  
Db 616 CTATGTTAACTTTACATGATACAGATCTTCGGGGACTTGTCTTACATTCACAATGTTGC 675  
Qy 617 TGGTGTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCCACACCCATCA 676  
Db 676 TGGAGTTGTACAGAGATCTAAAGCTCBAATCTTCTGTTGATCTCTTACTCATCA 735  
Qy 677 GTGTAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGTTGTAAGAGTGAAACCAAAATATC 736  
Db 736 AGTCAAAATCTGTGACTTTGGGAGTCGGAACAGCTCGTTAAAGGTGAAGCCAAATTTTC 795  
Qy 737 ATATATCTCTCTCGGTATATACCGAGCTCCAGAACTCATCTTTTGGTGCCACAGAGTATAC 796  
Db 796 TTACATCTCTCACGATTTACCGTGCAACCCGAGCTCATATTTGGTGCCACAGTATAC 855  
Qy 797 ATCATCAATGATATGCTGTGCTGTGTTCTTGGCAGAGCTACTTCTTGGGCAGCC 856  
Db 856 AACTTCTATGATATCTGCTGTGCTGTGTTCTTGTCTGAGCTTCTTCTTGGTCAGCC 915  
Qy 857 GTTATTCGGGAGAAATCTGTGCAACAGCTAGTGGAGATCATAAAGTTCTTTGGTAC 916  
Db 916 ATTATTTCCGGGAGAAATGCTGTGATCAGCTCGTTGAAATTTATAAAAGTTCTTGGTAC 975  
Qy 917 TCCAACTCCGAGAAATCGGTGCAATGAAACCAACTACACAGACTTCAGATTTCCCA 976  
Db 976 ACCAACTCGAGAAATCGGTGTATGAATCCATTTACACAGATTTTCAAGTTTCCCA 1035  
Qy 977 AATCAAGGCCACCTTGGCATAGGTTTTCACAAAGCGGATGCCCTCCGGAAGCCATTGA 1036  
Db 1036 GATAAAGGCACATCCCTGGCACAAGATCTTCACAAAGAGTGCCCCAGAGCGATGA 1095  
Qy 1037 CTTGATCTCGCTCTTCAATATCTCAACAGTCTACGTTGCACTGCGCTCGAGGCATG 1096  
Db 1096 TTTTGATCAAGGCTGTTCAATCTCTCAAGTCTAAGATGACACAGCGCTCGAAGCTTG 1155  
Qy 1097 TGGGATCCGTTTTCATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCGGCC 1156  
Db 1156 TGACATCCGTTCTTGTGATGAACTCAGAGAACCAACGCTCGTTTACCAAAATGGAGCGCC 1215  
Qy 1157 TCTACACACGCTTCTTCAACTTCAAAAGAGTGTCTGGGGCTTACCGGAGCTTATCAA 1216  
Db 1216 TTTCCGCTCTCTTCACTTCAAAAGAGTGTGTGATCATCACTGAACTGTGTCAA 1275  
Qy 1217 CAGGCTAAACAGAGATGTGAGGCGACAGATGAATGGTGGCTTTCCATTTCAAGCTGG 1276  
Db 1276 CAAGTTGATTCAGACCATATCAAGAGACAAATGGGTCTAAGCTTCTTGAATCAATCTGG 1335  
Qy 1277 ACCCTAGAA 1285  
Db 1336 AACTTAAAA 1344

RESULT 4

US-09-938-842A-875  
; Sequence 875, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 875  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-875

Query Match 44.7%; Score 730.8; DB 9; Length 1143;  
Best Local Similarity 77.5%; Pred. No. 2.1e-133;  
Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

Qy 141 ATAGACAAACGACAAAGAAATGTCTGCTGTATATAGAGGAAATGATGCTGTACCCTG 200  
Db 1 ATGGCTGATGATAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGCT 60  
Qy 201 CACATAATTTCTACTACAAATGAGGCAAAAATGTTGAACCTTAAACAGACCAATTAAGTTAC 260  
Db 61 CATATTTATTTCCACCACAAATCGGTGCAAAAATGGTGAACCAAAAACAGACAAATTAAGTTAC 120  
Qy 261 ATGGCGGAACGTGTTGTTGGAAACAGATCATTTCCGNAATTTGTTATTCAGGCAAAATCCTTG 320  
Db 121 ATGGCGGAGCGAGTTGTTGGTACAGCTCGTTCCGGATCGTTTCCAGCAAAATGTTTG 180  
Qy 321 GAACTTGGAGAAATCAGTAGCCATTAAGAAAGTTTTCAGAGATCGCCGTTTATAAAAAACCGA 380  
Db 181 GAGACTGGAGAAACCGTGGCGATTAAGAAAGTTTTCAGAGATAGAAGATACAGAACCGA 240  
Qy 381 GAGTTGCAATTAATGCGACTAATGGACCATCAAAATGTGGTTTCTTCCTTGAAGCAATTTGTTTC 440  
Db 241 GAACTTCACTGATGCTGTGATGATCATCCGAATGTGGTTTGTGTTGAAGCAATTTGTTTC 300  
Qy 441 TTCTCTCAACACTAGAGATGAGCTCTTCTCAATCTGTTTATGAGATGTACACAGAG 500  
Db 301 TTTTGCAGTACAAGTAAAGACGAGCTTTTCTTGAACCTTGGTTATGAGATGTGTCCTGAG 360  
Qy 501 ACATTTGATCCGGGTTTGAAGCACTATATAGTTTCAAAACAGCGGATGCTATCTTCTAT 560  
Db 361 AGCTTGTATGAGTTCTGAAACATATATAGTAGTGCAACCAAGAAATGCTCTTGTCTAT 420  
Qy 561 GTCAAACTTTACATACATAACCAATCTTTCAGAGGCTTGGCTTATATCATACTGCTCTGCT 620  
Db 421 GTTAAACTTTACATGATCAGATCTTCCGGGACTTGTCTTACATTCACAAATGTTGTGGA 480  
Qy 621 GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACCCCACTCAAGTGT 680  
Db 481 GTTTGTCAAGAGATCTAAAGCCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTC 540  
Qy 681 AAGCTCTGTGATTTTGGAAAGTGCAAAAGTACTGGTGAAAGGTGAACCAACCATATCATAT 740  
Db 541 AAAATCTGTGACTTTGGCAGTGGAAACAGCTCGTTAAAGGTGAAGCCAAACATTTCTTAC 600  
Qy 741 ATCTGCTCTCGGTATTAACCGAGCTCAGAACTCATCTTTGGTGCCACAGAGTATACATCA 800  
Db 601 ATCTGCTCAGATTTTACCGTGCCACCGAGCTCATATTTGGTGCCACTGAGTACACAACT 660  
Qy 801 TCCATTTGATATATGCTGCTGCTGTTGTTCTGCGAGAGCTACTTCTTGGGAGCGGTTA 860  
Db 661 TCTATTGATATCTGGTCTGCTGCTGTTCTTGTGCTGAGCTTCTTCTTGGTCAAGCATTA 720  
Qy 861 TTCCCGGAGAGAAATTTCTGTGGACACAGCTAGTGGAGATCATAAAGGTTCTTGTGATCTCCA 920  
Db 721 TTTCCCGGAGAGAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAGTTCTTGTGTACACCA 780  
Qy 921 ACTTCGGAAGAAATCCGGTGCATGAACCAAACTACACAGCTTCAGATTTCCCAAAATC 980  
Db 781 ACTCGAGAGAAATCCGGTTGTATGAATCCACATTCACAGATTTTCCAGGTTTCCACAGATA 840  
Qy 981 AAAGCCCAACCTTGGCATAAAGTTTTCACAGCGGATGCTCCGGAAGCATTTGACCTT 1040  
Db 841 AAGGCACATCCCTTGGCACAAGATCTTCCCAAAAGGATGCCCCCAAGAGGATTTGATTTT 900



QY 1041 GCATCTCGGCTTCTTCAATACCTACCAAGTCTACGTTGCACTGCGCTCGAGGCATGTGG 1100  
DB 901 GCATCAAGGCTGCTTCAATACCTTCTCAAGTCTAAGATGACAGCGCTCGAAGCTTGTGCA 960  
QY 1101 CATCGGTTTTTCAATGAACCTCGGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACCTCTA 1160  
DB 961 CATCGGTTTTTCAATGAACCTCAGAGAACCAACGCTCGTTTACCAATGGACGGCTTTC 1020  
QY 1161 CCACGGTTGTTCAACTTCAAAACAAGATGTCTGGGGCTTCCACCGAGCTTATCAACAGG 1220  
DB 1021 CCGCCTCTCTTCAACTTCAAAACAAGATGTCTGGGATCATCACTGAACTGGTCAACAG 1080  
QY 1221 CTAATACACAGACATGTGAGGCGACAGATGAATGCTGCTTCCATTTCAAGCTGACCC 1280  
DB 1081 TTGATTCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGGAAT 1140  
QY 1281 TA 1282  
DB 1141 TA 1142

RESULT 5  
US-09-938-842A-875  
; Sequence 875, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 875  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-875

Query Match 44.7%; Score 730.8; DB 11; Length 1143;  
Best Local Similarity 77.5%; Pred. No. 2.1e-133;  
Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

QY 141 ATAGCAACGACCAAGGAATGTCTGCTGTTATAGAGGAATGATGCTGTACCGGT 200  
DB 1 ATGGCTGATGATAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGT 60  
QY 201 CACATAATTTCTACTACAAATTTGAGGCAAAAATGGTGAACCTTAAACAGACCAATTAAGTTAC 260  
DB 61 CATATATTTTCCACCACCAATCGTGGCAAAAATGGTGAACCAACACAGCAATTAAGTTAC 120  
QY 261 ATGGCGGAACGTTGTTGGAAACAGATCATTCGGAATGTATTCAGGCAAAATGCTTG 320  
DB 121 ATGGCGGACGAGTTGTTGGTACAGGCTGTTTCGGGATCGTTTCCAAAGCAAAATGTTTG 180  
QY 321 GAACTGGAGATCAGTACGCAATTAAGAGGTTTTCAGATCGCGGTATTAABAAACCGA 380  
DB 181 GAGACTGGAGAACCGTGGCGGATAAGAGGTTTTCAGATAGAGATACAGAACCGA 240  
QY 381 GAGTTGCAATTAATGCAATTAATGGACCAATCAAAATGTTGTTTCCCTGAAGCATTTGTTTC 440  
DB 241 GAACTTCAGTTGCTGATGATGATCATCCGAATGTTGTTTGAAGCATTTGTTTC 300  
QY 441 TTCTCTACAAACGATAGATGAGCTCTTCTCTCAATCTCGTTATGGATGATGTACACAG 500

## RESULT 6

US-10-424-599-124786  
; Sequence 124786, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kowalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599

DB 301 TTTTGCATCAAGTAAGACGAGCTTTCTTGAACCTTGGTTATGAGATATGCTCCTGAG 360  
QY 501 ACATTTGATCCGGTTTTTGAAGCACTATATAGTTTCAAAACCGCGGATCCCTATCTTCTAT 560  
DB 361 AGCTTGTATCGAGTTCTGAACATTTATAGTAGTCAAAACCAAGAAATGCTCTTCTCTAT 420  
QY 561 GTCAAACTTTACACATCAAAATCTTCAAGAGCTTGGCTTATATCCATATCTGCTCTGCT 620  
DB 421 GTTAAACTTTATCATGTATCAGATCTTCCGGGACCTTGTCTATCATTAATCACAATGTTCTGGA 480  
QY 621 GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACACCATCAGTGT 680  
DB 481 GTTGTTCAGAGATCTAAAGCTCAAAATCTTCTGGTTGATCCCTTCTACTCATCAAGTC 540  
QY 681 AAGCTCTGTGTATTTTGGAAAGTGCAAAAGTACTGTGTGAAGGTGAACCAAAATATCATAT 740  
DB 541 AAAATCTGTGACTTTGGCAGTTCGGAACAGCTCGTTAAAGGTGAAGCCAAATTTCTTAC 600  
QY 741 ATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTTGGTGCCACAGATATACATCA 800  
DB 601 ATCTGCTCAGCATTTCTACCGTGCACCCGAGCTCATATTTGGTGCCACTGAGTACACAACT 660  
QY 801 TCCATTGATATATGCTGCTGCTGTTGCTTCTGCGAGAGTACTTCTTTGGGCGAGCGTTA 860  
DB 661 TCTATTGATATCTGCTGCTGCTGTTGCTTCTGCTGAGCTTCTTCTTGGTGAGCCATTA 720  
QY 861 TTCCCGGAGAAATTTCTGTGGAACAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCA 920  
DB 721 TTTCCCGAGAAATGCTGTGATCAGCTCGTTGAAATTAATAAAGTTCTTGGTACACCA 780  
QY 921 ACTCGGAAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTTCCCAAAATC 980  
DB 781 ACTCGAGAAAGAAATCCGGTGTGATGAATCCACATTAACAGATTTTCAAGTTTCCACAGATA 840  
QY 981 AAAGCCCACTTGCATAAGGTTTTTCCACAGCGAGTCCCTCCGGAAGCCATTCACACTT 1040  
DB 841 AAGGCACATCTCCGTCGCAAGATCTTCCAAAGAGATGCCCCCAAGAGCGATTTGATTTT 900  
QY 1041 GCATCTCGGCTTCTTCAATATCTACCAAGTCTACGTTTGCACCTCGGCTCGAGCATGTGG 1100  
DB 901 GCATCAAGGCTGCTTCAATATCTTCCAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA 960  
QY 1101 CATCGGTTTTTCAATGAACCTCGGTGAGCAAAATGCTGCTTCCAAATGGCGGACCTCTA 1160  
DB 961 CATCGGTTTTTGTATGAATCAGAGAACCAACGCTCGTTTACCAAAATGGACGGCTTTC 1020  
QY 1161 CCACGGTTGTTCAACTTCAAAACAGAGTTGTCTGGGCTTCCACCGAGCTTATCAACAGG 1220  
DB 1021 CCGCCTCTCTTCAACTTCAAAACAGAGATGATGCTGGATCATCACCTGGAATGTTGCAACAG 1080  
QY 1221 CTAATACACAGCATGTGAGGCGACAGATGAATGTTGGCTTTTCCATTTCAAGCTGGAACCC 1280  
DB 1081 TTGATTCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGGAAT 1140  
QY 1281 TA 1282  
DB 1141 TA 1142

QY	1026	GAAGCCATTGACCTTGCATCTCGGCTTCTTCAATACTACCAAGTCTACGTTGCACCTGGC	1085
DB	1675	GAAGCAATTGACCTTGCATCAAGGCTTCTCCAATATTACCTAGTCTACGCTGCACCTGGC	1734
QY	1086	CTCGAGGCATGTGCGCATCCGTTTTTCAATGAACCTCCGTGAGCCAAATGCTCGTCTTCCCA	1145
DB	1735	CTGGAAGCATGTGCAATCTCTTCTTTGATGAGCTTCGGAGCCAAATGCCCGTCTTCCT	1794
QY	1146	AATGGCCGACCTCTACACACCGTTGTTTCAACTTCAAAACAAGAGTTGTCTGGGGCTTCACCG	1205
DB	1795	AATGGCATCCACTGCCCCCACTTTTCAACTTCAACAGGAGTTAGCTGGAGCATCACCT	1854
QY	1206	GAGCTTATCAACAGGCTAATACACAGAGCATGTGAGGCGACAGATGAATGTTGGCTTTCCA	1265
DB	1855	GAACTGATCAATAGGCTCATCCAGAGCATATTAGCGCGCAGATGGGTCTCAGCTTCCCG	1914
QY	1266	TTTCAAGCTGGACCCCTAGA	1284
DB	1915	CATTCTGCCGGTTTCATAGA	1933
RESULT 7			
US-10-292-408-15			
; Sequence 15, Application US/10292408			
; Publication No. US20030182692A1			
; GENERAL INFORMATION:			
; APPLICANT: VAN THIELEN, NOCHA			
; APPLICANT: DA COSTA E SILVA, OSWALDO			
; APPLICANT: CHEN, RUOYING			
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS			
; TITLE OF INVENTION: OF USE IN PLANTS			
; FILE REFERENCE: 16313-0178			
; CURRENT APPLICATION NUMBER: US/10/292,408			
; CURRENT FILING DATE: 2002-11-12			
; PRIOR APPLICATION NUMBER: 60/346,096			
; PRIOR FILING DATE: 2001-11-09			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 15			
; LENGTH: 1621			
; TYPE: DNA			
; ORGANISM: Brassica napus			
US-10-292-408-15			
Query Match 43.3%; Score 709; DB 16; Length 1621;			
Best Local Similarity 76.8%; Pred. No. 4.5e-129;			
Matches 868; Conservative 0; Mismatches 285; Indels 0; Gaps 0;			
QY	161	GTCTGCTGCTGTATTAGAAGAAATGATGCTGTATCCGGTCAATATTTCTACTACAAT	220
DB	155	GCGCGTCTGTAGTTGATGCATGACCAAGTCACTGGCCACATAATCTCCACCACAT	214
QY	221	TGAGGCAAAATGTGTGAACCTAAACAGACATTAAGTTACATGCCGAAAGTGTGTGG	280
DB	215	CGTGTGTAAACCGAGAACCAAAACAGACAATAAGTTACATGCGGAGCGAGTGTGCG	274
QY	281	AACAGGATCATTCCGGAATGTTATCCAGGCAAAATGCTTGGAACTCGGAATCAGTAGC	340
DB	275	TACAGGCTCTCTCGGGAATGTTTCCAGGCGAAGTGTCTGGAGACTGGAGAAACCGTGGC	334
QY	341	CATTAGAAGAGTTTTCGAAGATCGCCGTTATAAAACCGAGAGTTGCAATTAATTCGCACT	400
DB	335	GATAGAAGAGTTTTCGAACAGAGGAGTTACAGAACCGAGAGCTTCAGCTGATGCGTGT	394
QY	401	AATGGACCATCCAAATGTGTTTCTTTGAAGCAATGTTTCTTCTCTCAACAGCTAGAGA	460
DB	395	GATGGACCATCCGAAATGTTGTTTGAAGCAATGTTTCTTCTCGACCAACGAGCAAGA	454
QY	461	TGAGCTCTTCTCAATCTCGTTATGGAGTATGATACAGAGACATTTGTACCGGTTTCAA	520
DB	455	CGAGCTGTTTCTGAACCTTGGTTATGGAGTATGTCCTTGAGAGCTTGTACCGAGTCTGAA	514



Db 1073 ACTGCATTGAAGCATGTGCACATCCTTTCTTTGATGAACCTTGGTGAACCCAAACGCTCG 1132  
Qy 1140 CTTCCAAATGGCGAGCTCTACACCGTTGTTCAACTTCAAAAGAGTTGCTGGGCT 1199  
Db 1133 CTGCCAAATGGTCGCCCAATTTCCCTCTATTTAACTTCAACAGGAATTTATCTGGAGCA 1192  
Qy 1200 TCACCGGAGCTTATCAACAGGCTTAATACAGAGCATGTGAGGCGACAGATG 1250  
Db 1193 TCTCCGAGCTTGTAAATAGTTGATACCTGACCATGTGAGGCGCAATG 1243

RESULT 9  
US-10-425-114-12807  
; Sequence 12807, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, Steven E.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 12807  
; LENGTH: 1726  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701212714\_FLI  
US-10-425-114-12807

Query Match 43.2%; Score 707; DB 18; Length 1726;  
Best Local Similarity 76.6%; Pred. No. 1.1e-128;  
Matches 866; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Qy 120 TCTTTGAAAGCTCGTCCGATATAGACAACGACAAGAAATGCTGCTGTATAGAA 179  
Db 71 TCTCTCTCTCTCCCTCCGCTGCTGAGGATAAGAGATGCTACCTCTGTCAAT 130  
Qy 180 GGAATATGATCTCTTACCGCTACATAATTTCTACTACAAATCGAGCGCAAAATGTGAA 239  
Db 131 GGAATATGATCTCTTACCGCTACATAATTTCTACTACAAATCGAGCGCAAAATGTGAA 190  
Qy 240 CCTAAACAGACATTTAGTTACATGGCGGAAACGTTGTTGGAAACAGGATCATTCGGAAT 299  
Db 191 CCCAAACAGACATTTAGTTACATGGCGGAAACGTTGTTGGAAACAGGATCATTCGGAAT 250  
Qy 300 GTATTCAGGCAAAATGCTTGGAAACGTTGGAAATCAGTAGCCATTTAAGAGGTTTGGCAA 359  
Db 251 GTTTTCCAGGCAAAATGCTTGGAAACGTTGGGAGGAGGAGGCAATTTAAAGAGTTTACAA 310  
Qy 360 GATCGCGGTTATAAACAGAGGTTGCAATTAATCGACTAATGACCATCCAAATGTCG 419  
Db 311 GACAGAAGATACAGAATGTGAATGCAATTAATCGGTTGATGATCAATCAATATG 370  
Qy 420 GTTTCTCTTGAAGCATTTGTTCTTCTTCAACGACTAGAGATGAGCTTCTCTCAATCTC 479  
Db 371 ATCTTTTGAAGCATTTGTTCTTCTTCAACGACTAGAGATGAGCTTCTCTCAATTTG 430  
Qy 480 GTTATGAGATGTATGACAGAGACATTTGACCGGTTTGAAGCACTATAGTTCAAAAC 539  
Db 431 GTGATGAGATGTATGACAGAGATCCATGTATAGAGTCTTAAAGCACTATAGCAATGCTAAT 490  
Qy 540 CAGGAGATGCTATCTCTATGTCAACTTTTACATACCAATCTTCAGAGCTTGGCT 599  
Db 491 CAAAGATGCAATCATCTTACGTTAAACCTTTATATGACAGATTTTCAGGGGTTGGCT 550  
Qy 600 TATATCCATATGCTCTCTGCTGTGTCACAGAGATATAAAACCAAAATCTTTTGGTT 659

Db 551 TACATCCACACTGGTCCCAAGTTTGGCACAGATTTGAAGCCTCAAAATATATCTGGTG 610  
Qy 660 GATCCCCACACCCATCAGTGTGAAGCTCTGTGATTTTGGAGTGCAAAAGTACTGGTAA 719  
Db 611 GATCTCTTTACACACCAAGTGAAGCTATGTGATTTTGGAGTGCAAAAGTCTTAGTCGAA 670  
Qy 720 GGTGAACCAACATATCATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTT 779  
Db 671 GGTGAAGCTTAT 730  
Qy 780 GGTGCCACAGAT 839  
Db 731 GGGGCGCACAGATATACAGTTCCGATTTGATATTTGGTCAAGTGGCTGTCTTGTCTGAA 790  
Qy 840 CTACTTCTTGGCGAGCGGTTATTTCCGGGAGAAATTTCTGTGACAGCTAGTGGAGATC 899  
Db 791 CTTCTTTTGGGCGAGCCATTTATTTCCCTGGCGAAATGTCAGTAGACAGCTTTGTACATA 850  
Qy 900 ATAAAGGTTCTTTGGTACTCCAACTCGCGAAGAAATCCGGTGCATGAACCCAAACTACACA 959  
Db 851 ATAAAGTCTTTGGCACACCCACCCGAGAGAGTACGCTGTATGATCCCAATTACAT 910  
Qy 960 GACTTCAGATTTCCCAAAATCAAAAGCCACCTTGGCATPAAGTTTTCACAAGCGGATG 1019  
Db 911 GACTTTAGGTTTCCACAGATAAAAGCACACCCATGSCACAGATATTCACAAAAGATG 970  
Qy 1020 CTTCCGGAAGCATTTGACCTTGCATCTCGGCTTCTTCAATCTCACCAGTCTACGTTGC 1079  
Db 971 CTTCCGGAAGCATTTGATCTTGCATCTCGGCTTTCGCAATATCTCCCAAGTCTCCGGTGC 1030  
Qy 1080 ACTGCGCTCGAGCATGTCGATCGTTTTCATGAACTCGTGAGCAAAATGCTCGT 1139  
Db 1031 ACTGCGCTTGAAGCATGTCACATCTTCTTTGATGAACCTTGGTGAACCTTAATGCTCGC 1090  
Qy 1140 CTTCCAAATGGCGACCTCTACACCGTTTTCATCTTCAAAACAGAGTTGCTGGGCT 1199  
Db 1091 TTTGCCAAATGGTCTGCTCAATTTCCCTCTTATTTAACTTCAACAGGAATATCTCGAGCA 1150  
Qy 1200 TCACCGGAGCTTATCAACAGGCTATACAGAGCATGTGAGGCGACAGATG 1250  
Db 1151 TCTTCGAGCTTGTTAATAGTTGATCTGACCTGACCATGTGAAGCGGCAATG 1201

RESULT 10  
US-10-424-599-67990  
; Sequence 67990, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 67990  
; LENGTH: 1979  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_32408C.1  
US-10-424-599-67990

Query Match 43.2%; Score 707; DB 18; Length 1979;  
Best Local Similarity 76.6%; Pred. No. 1.2e-128;  
Matches 866; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Qy 120 TCTTTGAAACGTCGTCCGATATAGACAACGAAATGCTGCTGTATAGAA 179

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Db 289 TCTCTCTCTCCCTCCGCTGAGGATAAGGAGATGCTACCTCTGTCTCATCAAT 348
QY 180 GGAATGATGCTGTACCGGTACATATTTCTCTACATTTGGAGGCAAAATGGTGAA 239
Db 349 GGGAAATGATTCCTTAATGCTGATCATATCTATCTACAACTATTGGAGGCAAAATGGGAA 408
QY 240 CTTAAACAGACATTTAGTTTACATGCGCAACGTTGTTGGAACAGGATCATTCGGAATT 299
Db 409 CCCAAACAGACTTTAGCTACATGCGAGAACCGGTTGTAGGAACCTGGATCATTTGGAATC 468
QY 300 GTATTCCAGGCAAAATGCTTGGAACTGGAGAACTCAGTAGCCATTAAGAAGGTTTGGCAA 359
Db 469 GTTTTCCAGGCAAAATGCTTGGAACTGGAGGAGGAGTGGCAATTAAGAAGGTTTTCACAA 528
QY 360 GATCGCGTTATAAAACCGAGAGTTGCAATTAATGCGACTAATGAGCAATCCAAATGTG 419
Db 529 GACAGAAGATACAAGAACTCGTAACCTGCGAGTTTAATGCGGTGTGATGATCATCCAAATGTG 588
QY 420 GTTTCCTTGAAGCATTTGTTCTTCTCAACAGACTAGAGATGAGCTCTTCTCAATCTC 479
Db 589 ATCTCTTTGAAGCATTTGTTCTTCTCAACACTACAAGTACAGATGAACCTTTTCTCAATTTG 648
QY 480 GTTATGGAGTATGTACACAGACATTTGTACCGGGTTTGAAGCACTATATACTAGTTCAAAAC 539
Db 649 GTGATGGAGTATGTTCAGAGTCCATGTATAGAGTCTTAAGCACTATAGCAATGCTAAT 708
QY 540 CAGCGGATGCTTATCTTCTATGTCAAACTTTACATACCAAAATCTTCAGAGGCTTGCTG 599
Db 709 CAAAGAATGCCAATCATCTACCTGTAACCTTTATATGTACCAAGATTTTCAGGGGGTTGGCT 768
QY 600 TATATCCATACGCTCTGCTGCTGCGCACAGATATAAACCAAAATCTTTTGGTT 659
Db 769 TACATCCACACTGGTCCCAAGTTTGGCCACAGAGATTTGAAGCCCTCAAAATATATCTGGTG 828
QY 660 GATCCCCACACCCATCAGTGAAGTCTGTGATTTTGGAAAGTGCAAAAGTACTGCTGGA 719
Db 829 GATCTCTTACACACCAAGTGAAGTATGTGATTTTGGAGTGCAAAAGTCTAGTCCGAA 888
QY 720 GGTGAACCAACATATATATCTGCTCTCGGTATTAACCGAGTCCAGAACTCATCTTT 779
Db 889 GGTGAAGCTAATATATATATATATGTTTCAAGTCTATCGAGCACCAAGACTTATATTT 948
QY 780 GGTGCCACAGATATACATCATCAATGATATATGCTGCTGCTGTTGTTCTGCGCAG 839
Db 949 GGGGCCACAGAGTATACCAATGTCGATGATATTTGCTGAGTGGCTGCTGTTCTGCTGAA 1008
QY 840 CTACTTCTTGGCGACCGTTATTTCCGGGAGAAATTTCTGCGACAGCTAGTGAGATC 899
Db 1009 CTTCTTTTGGCGACCCATTTATCTCGGGAATATGAGTAGACAGCTTGATGATATTT 1068
QY 900 ATAAAGGTTCTTGGTACTTCCAACTCGCAAGAAATCCGGTGATGAACCCCAAACTACACA 959
Db 1069 ATAAAGGTTCTTGGCACACCCACCCGAGAGGAGTACGCTGTATGAATCCCAATTTACAAT 1128
QY 960 GACTTCAGATTTCCCAAAATCAAGCCACCCCTTGGCATTAAGTTTTCACAGCGGATG 1019
Db 1129 GACTTTAGGTTTCCACAGATAAAGCACACCCATGGGCAAGATATCCCAAAAGATG 1188
QY 1020 CTTCCGGAAGCATTTGACTTGCATCTCGGCTTCTTCAATCTACACCAAGTCTAGCTTGC 1079
Db 1189 CTTCCAGAAAGCTTTTGAATCTTGCATCTCGGCTTCTTGAATCTCCCAAGTCTCGGTGC 1248
QY 1080 ACTGCGCTCGAGGCAATGTGCGCATCCGTTTTCATGAATCTCGTGAGCCAAATGCTCGT 1139
Db 1249 ACTGCGCTTGAAGCATGTGCATCTTCTTTGATGAATCTCGTGAACCTTAATGCTCGC 1308
QY 1140 CTTCCAAATGGCGGACCTTACACCGTTTGTTCAACTTCAAAAGAGTTGTCTGGGGCT 1199
Db 1309 TTGCCAAATGGTGTGCTCCATTTTCCCTCTTATTTAACTTCAAAAGAGATTTATCTGGAGCA 1368
QY 1200 TCACCGGAGCTTTATCAACAGGCTTATACAGAGCATGTGAGGCGCAGATG 1250
Db 1369 TCTCCGAGCTTGTGTAATAAGTTGATACCTGACCAATGTGAAGCGGCAATG 1419

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RESULT 11
US-10-292-408-21
; Sequence 21, Application US/10292408
; Publication No. US20030182692A1
; GENERAL INFORMATION:
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: DA COSTA E SILVA, OSWALDO
; APPLICANT: CHEN, RUOYING
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
; FILE REFERENCE: 16313-0178
; CURRENT APPLICATION NUMBER: US/10/292,408
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/346,096
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1499
; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-21

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Query Match 43.1%; Score 705; DB 16; Length 1499;
Best Local Similarity 77.1%; Pred. No. 2.7e-128;
Matches 858; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

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QY 136 CCGATATAGACACGACAAAGGAAATGCTGCTGCTGTTATAGAGGAATGATGCTGTTA 195
Db 159 CCGAGCCGCGCACGAAAGGAATGTCAGCTCTGTCGAGATGTAATGATGACTCA 218
QY 196 CCGGTACATATTTCTACTACAAATGGAGGCAAAATGGTGAACCTAAACAGACCATTA 255
Db 219 CTGGTACATATCTCAACCAATTTGAGGCAAAATGGCGAACCTAAACAAACCATCA 278
QY 256 GTTACATGCGCAAGCTGTTGTTGGAACAGATCATTCGGAATGTTATTCAGGCAAAAT 315
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QY 316 GCTTGGAACTGGAGAACTAGTACCAATTAAGAGGTTTTCGCAAGATCGCGTTATAAAA 375
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Db	1076	GTGCACATCCTTTCTTTGATGAATTCGAGAACCCCAATGCTGCGCTGCCAAATGGTCGTC	1135
Qy	1156	CTCTACCAACGTTGTTCAACTTCAACAAAGAGTTGCTGGGGCTTCACCGGAGCTTATCA	1215
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:16:02 ; Search time 8124.57 Seconds  
(without alignments)  
7664.793 Million cell updates/sec

Title: X94938  
Perfect score: 1636  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.4	58.0	1409	3	CNS0ABFT
2	949.4	58.0	1461	3	CNS0AB1V
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4	689.8	42.2	1197	9	CL957492
5	684	41.8	1745	3	AY106255
6	680.4	41.6	684	5	BP560588
7	673.2	41.1	690	1	AV782869
8	660.2	40.4	683	5	BP560678
9	654.6	40.0	1666	1	AY104068
10	620	37.9	658	1	AV822185
11	615	37.6	924	7	CK266410
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13	598.2	36.6	1967	3	AY103345
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16	572.2	35.0	932	7	CV290871
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18	563.2	34.4	595	1	AY1993897
19	562.6	34.4	910	7	CK290108
20	562.4	34.4	829	6	CB971865
21	560	34.2	1604	3	CNS0A4PT
22	558.8	34.2	1752	3	AY108486
23	548	33.5	963	7	CK286429
24	546	33.4	666	6	CD824216

25	546	33.4	821	6	CB894470
26	544.2	33.3	952	7	CK289285
27	542.2	33.1	944	7	CK290066
28	538.4	32.9	1870	3	CNS0ADOL
29	538	32.9	887	6	CD574542
30	537.8	32.9	2036	3	CNS0A425
31	533.8	32.6	876	7	CF208184
32	529.4	32.4	1667	3	CNS0A5F6
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35	526.2	32.2	727	6	CD815282
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43	504.8	30.9	790	7	CO107864
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## ALIGNMENTS

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ACCESSION	BX815323	1	GI:42471412		
VERSION	HTC; GSLT cDNA				
KEYWORDS	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.				
AUTHORS	Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 1409)				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (18-NOV-2003) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)				
JOURNAL	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length				
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QY	877	CTGTGACAGCTAGTGGAGATCATAAAGTCTCTGCTACTCCAACTCGCGAAGAAATCC	936
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CNS0ABIV

1461 bp mRNA linear HTC 06-PEB-2004

Arabidopsis thaliana Full-length cDNA Complete sequence from clone

GSLTSL422C04 of Silique of strain col-0 of Arabidopsis thaliana

(thale cress).

BX817800

HTC; GSLT cDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1461)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

Unpublished

2 (bases 1 to 1461)

Genoscope.

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

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FEATURES  
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Best Local Similarity 85.8%; Pred. No. 4.7e-181;
Matches 1079; Conservative 0; Mismatches 171; Indels 7; Gaps 2;

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VERSION AV782577
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 709)
AUTHORS Seki.M., Narusaka.M., Ishida.J., Kamiya.A., Satou.M., Nakajima.M.,
Oono.Y., Sakurai.T., Carninci.P., Kawai.J., Itoh.M., Ishii.Y.,
Arakawa.T., Shibata.K., Shingawa.A., Muramatsu.M., Hayashizaki.Y.
and Shinozaki.K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meeki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
further details.

FEATURES
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ORGANISM      Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 684)
AUTHORS      Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
      Nakajima,M., Enju,A., Kiyama,K., Oono,Y., Muramatsu,M.,
      Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
      Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
      Functional annotation of a full-length Arabidopsis cDNA collection
      Science 296 (5565), 141-145 (2002)
TITLE      Science 296 (5565), 141-145 (2002)
JOURNAL
MEDLINE
PUBMED
PUBMED      11910074
COMMENT      Contact: Motoaki Seki
      Plant Functional Genomics Research Group
      RIKEN Genomic Sciences Center
      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
      Tel: 81-298-36-4359
      Fax: 81-298-36-9060
      Email: msek@rtc.riken.go.jp
      Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
      further details.
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      QY      774 ATCTTTGGTGCACAGAGTATACATCCATTGATATATGCTCTGCTGTTGTTCTG 833
      Db      1 ATCTTTGGTGCACAGAGTATACATCCATTGATATATGCTCTGCTGTTGTTCTG 60
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      Db      61 GCAGAGTACTTCTTGGGAGCGTTATTCCTGGGAGAAATTTCTGTGACGAGTAGTG 120
      QY      894 GAGATCATAAAGTCTTGTGCTACTCAACTCGCGAAGAAATCCGCTGCATGACCCAAAC 953
      Db      121 GAGATCATAAAGTCTTGTGCTACTCAACTCGCGAAGAAATCCGCTGCATGACCCAAAC 180
      QY      954 TACACAGACTTTCAGATTCCCAAAATCAAGCCACCCCTTGGCATGAAGGTTTTCCACAAG 1013
      Db      181 TACACAGACTTTCAGATTCCCAAAATCAAGCCACCCCTTGGCATGAAGGTTTTCCACAAG 240
      QY      1014 CGATGCTCCGGAAGCATTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
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      QY      1074 CGTTGCACTCGCTCCGAGGAGTGGCGCATGCGGTTTTTCAATGAATCCGTGAGCCAAAT 1133
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Db      361 GCTCGTCTTCCAAATGCGCGACCTCTACACACGTTGTTTCAACTTCAAAACAGAGTTGTCT 420
QY      1194 GGGGCTTCCACGGAGCTTATCAACAGGCTAAATACACAGAGCATGTGAGGCGCAGAGTAAT 1253
Db      421 GGGGCTTCCACGGAGCTTATCAACAGGCTAAATACACAGAGCATGTGAGGCGCAGAGTAAT 480
QY      1254 GGTGGCTTTCCATTTCAAGCTGGACCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC 1313
Db      481 GGTGGCTTTCCATTTCAAGCTGGACCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC 540
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QY      1434 AATCAGAGGCGCATGATTTGTGTC 1457
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DEFINITION      mRNA sequence.
ACCESSION      AV782869
VERSION      AV782869.1 GI:19801659
KEYWORDS      EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 690)
AUTHORS      Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
      Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
      Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
      and Shinozaki,K.
      Large scale analysis of Arabidopsis full-length cDNA (2002b)
      Unpublished (2002)
      Contact: Motoaki Seki
      Plant Functional Genomics Research Group
      RIKEN Genomic Sciences Center
      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
      Tel: 81-298-36-4359
      Fax: 81-298-36-9060
      Email: msek@rtc.riken.go.jp
      An Arabidopsis full-length cDNA library was constructed essentially
      as reported previously (Seki et al., 1998). This clone is in a
      modified plasmid vector as a SstI/XhoI insert. Please visit our
      web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
      further details.
FEATURES
      source      1..690
      /organism="Arabidopsis thaliana"
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      /dev_stage="rosette plants"
      /lab_host="SOLR"
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      /note="Site 1: SstI; Site 2: XhoI; subjected to
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      Matches 686; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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AV104068  
LOCUS AV104068 1666 bp mRNA linear HTC 16-OCT-2002  
DEFINITION Zea mays PC0083097 mRNA sequence.  
ACCESSION AY104068  
VERSION AY104068.1 GI:21207146  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 1666)  
REFERENCE Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,  
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
AUTHORS Maize Mapping Project/DuPont Consensus Sequences for Design of  
TITLE Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 1666)  
AUTHORS Coe, E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones,  
these are publicly available from ZmDB and may be found by BLAST  
searching at WSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
Schnable, Iowa State, then clones may be requested from ZmDB:  
www.zmdb.iastate.edu.  
LOCATION/Qualifiers  
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assembled by DuPont as part of a collaboration for the  
overgo addressing of BACs in conjunction with the Maize  
Mapping Project"

ORIGIN  
Query Match 40.0%; Score 654.6; DB 3; Length 1666;  
Best Local Similarity 75.2%; Pred. No. 1.4e-121;  
Matches 816; Conservative 0; Mismatches 269; Indels 0; Gaps 0;  
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QY 237 GAACCTAAACAGACCAATTAGTTACATCGCGCAACGTTGTTTGGAAACAGGATCATTCGGA 296  
DB 320 GAGCCCAAGCGGACCATCAGTTACATGCGCAACGTTGCTGGTACGGGCTCATTTGGG 379  
QY 297 ATTGTTATCCAGGCAAAATGCTTTGGAAACCTGGAGATCAGTACCCATTAGAAGGTTTG 356  
DB 380 ATCGTCTTCCAGGCTAAGTGTTTGGAGACTGGAGACCTTCGCCATTAGAAGAGTGCTG 439  
QY 357 CAAGATCGCGGTTATAAACCCGAGAGTTGCAATTAATGCGACTAATGGACCATCAAAAT 416  
DB 440 CAGATCGCGGTTACAGAAACCGGAGCTCAACTTATGCTGCCATGGAGCACCCCAAC 499  
QY 417 GTGGTTTCCCTGAAGCAATGTTTCTTCTCTACACGACTAGAGATGAGCTCTTCCTCAAT 476  
DB 500 GTCATCTGCTGAAGCACTGCTTCTTCTCAACACGAGCAGGACGAGTTGTTCTTAAAC 559  
QY 477 CTGTTATGAGGATGTATGACAGACACATTTGACGGGTTTGAAGCACTACTACTAGTTCA 536  
DB 560 CTTGTGTCATGGAATTTGTCCTCCGAGACCTGTACCGTGTCTGAGCACTACAGCAACGGC 619

QY 537 AACACGCGGATGCCCTATCTTCTATGTCAAACCTTTACACATACCAAAATCTTCAGAGCGTTG 596  
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QY 657 GTTGATCCCCACACCCATCAGTGTAAGCTCTGTGATTTTGGAGTGCAAAAGTACTCTGGG 716  
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DB 800 CTTGTGTAACCGAACATATCTTACATATGCTCTCGTATTATATCGTGTCTCCAGAGCTCAT 859  
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LOCUS AV822185  
DEFINITION AV822185 658 bp mRNA linear EST 01-APR-2002  
AV822185 RAPL5 Arabidopsis thaliana cDNA clone RAFL05-02-L16 5',  
mRNA sequence.  
ACCESSION AV822185  
VERSION AV822185.1 GI:19864218  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
1 (bases 1 to 658)  
REFERENCE Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
AUTHORS Large scale analysis of Arabidopsis full-length cDNA (2002b)  
JOURNAL Unpublished (2002)

CONTACT: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msek@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a Sati/XhoI insert. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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Db	97	TGGGGCTCT	CAGCCTCCGCT	TTTAGCTCT	CAGCGCGGCAT	CTTCAGCGCGGAGATT	156
Qy	121	CTTTGAAAC	CGTCGTC	CCGATATAG	CAACGA	CAAGGAAATGTCTGCTGCTGTTTATAGAAG	180
Db	157	CTTTGAAAC	CGTCGTC	CCGATATAG	CAACGA	CAAGGAAATGTCTGCTGCTGTTTATAGAAG	216
Qy	181	GAATGATGCT	GTTACCGGT	CACATTA	TTTCTACT	CAATTTGGAGGCAAAAATGGTGAAC	240
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Qy	301	TATTCAGGCA	AAATGCTTTGGAAC	CTGGAGAA	TCAGTAGCAAT	TAAGAAGTTTTTCAAG	360
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Qy	361	ATCGCGCTT	ATAAAAAC	CGAGAGTTG	CAATTAATGCGCACT	TAATGGACCATCCAAATGTGCG	420
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Db	457	TTTCTCTGA	AGCATTTGTTCTT	CTACACG	CACTAGAGATG	AGCTCTTCTCCTCAATCTCG	516
Qy	481	TTATGGAGT	ATGTAC	CAGAGACATTTG	TACCGGGTTTTGAAGCACT	TATCTAGTTTCAAAAC	540
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Db	577	AGCGGATG	CTATCTTCT	TATGTCAAAC	TTTTACACATAC	CAAAATCTTCAGAGGCTTGGCTT	636
Qy	601	ATATCCAT	ATCTGCTCCT	GGTGT			622
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RESULT 11	REFERENCE
CK266410	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	COMMENT
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

**FEATURES**  
**SOURCE**

Location/Qualifiers

1. .924

organism="Solanum tuberosum"  
mol\_type="mRNA"  
cultivar="Kennebec"  
db\_xref="taxon:4113"  
clone="POAC457"  
tissue\_type="abiotic stress treated leaf and root tissue"  
lab\_host="DH10B-TonA"  
clone\_lib="potato abiotic stress cdna library"  
note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
supplier: Solanum tuberosum var. Kennebec plants were  
grown from cuttings on a 16hr light/8 hr dark cycle at 25  
C for 3-4 weeks. Biotic stress conditions were applied to  
four separate sets of plants. Set 1 involved saturation of  
the soil with 150 mM NaCl and tissues were harvested at  
following application of the salt stress (leaves: 2hr,  
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).  
Set 2 were grown under the standard conditions and then  
were water stressed by withdrawal of further watering  
applications. Drought stressed plants were harvested after  
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d  
and 5d). Set 3 were grown under the standard conditions  
and then were cold stressed by placement at 4 C. Cold  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
and 4d and roots were grown under the standard conditions and  
then were heat stressed by placement at 35 C. Heat  
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
2d and 4d and heat-stressed roots were harvested at 6 hr,  
12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
equal RNA from each tissue and stress was pooled to  
construct the cdna library. RNA sample."

## ORIGIN

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Qy	346	AGAAGGTTTTGCAAGATCGCGTTTATAAACCAGAGTTTGCAATTAAATCCGACTAATGG		405		
Dd	61	AGAAGGTTTTACAGGACACAGCGGTATAAAACCGTGAATCAACTGATCGCTTGATGG		120		
Qy	406	ACCATCCAATGTGGTTTTCTCTGAAGCATTTGTTCTTCTCACAAACGACTAGAGATGAGC		465		

Db	121	ATCACCAAAATGTCATTTACTCTAAAGCACTGCTCTTTTCCAGCACTAGTAGAGATGAGC	180
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Qy	526	ATACTAGTTTCAACACGCGATGCTCTATCTTCTATGTCAAACTTTTACACATACCAATCT	585
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Db	301	TCAGAGGCTGGCTTACATTAATGTTCCAAAGATTTGCCATAGAGATGTGAACCTC	360
Qy	646	AAATCTTTGGTTGATCCCAACCAACCATCATGTGTAAGCTCTGTGATTTTGAAGTGCAA	705
Db	361	AAATCTTTGGTTGATCTCTGACCCATCAAGTCAAGCTATGTGATTTTGAAGTGCAA	420
Qy	706	AGCTACTGGTGAAGGTGAACCAACATATCATATCTGCTCTCGTATTTACCGAGCTC	765
Db	421	AGTCTCTGGTGAAGGTGAAGCAATATTTCTGACATTTGCTCTCGTACTACAGAGCTC	480
Qy	766	CAGAATCTATCTTTGGTGGCCACAGAGTATACATCATCTGATATGATGCTGCTGGTT	825
Db	481	CAGAATCTATTTGGTGGCCACAGATATACATCATCAATTTGCTGACAGGCT	540
Qy	826	GTGTTCTGGAGAGTACTTTCTGGGAGCGGTTATTTCCGGGAGAAAATTTGTGGACC	885
Db	541	GTGTTCTGTGAGCTTTCTGGGAGCGGCTTTCTGGGAGAAAATTTGTGGAGACC	600
Qy	886	AGCTAGTGGAGATCAAAAGTTCTTGGTACTCCAACTCGGAGAAAATTTGTGGAGTGA	945
Db	601	AACCTGGTGGAGATCATCAAGTCTTGGTACTCTTACTCGGAGAAAATTTGTGGATGA	660
Qy	946	ACCAAACTACACAGACTTCAGATTTCCCAAAATCAAGCCCACTTGGCATTAAGGTTT	1005
Db	661	ACCAAACTACACAGATTTTCAGATTTCCCAAGATTAAGCTCATCTTGGCACAAGTAT	720
Qy	1006	TCACAAGCGGATGCTTCGGAAGCCATTTGACCTTGATCTCGGCTTCTCAATATCTAC	1065
Db	721	TCATATAAAGAAATGCTCTCTGAAGCAATTTGATCTGCTCAGCGCTTCTCAATATTCAC	780
Qy	1066	CAAGTCTACGCTGCTGCTGCGGAGCATGCGCATCGTCTTTCATTAAGTACTCGTG	1125
Db	781	CAAGTCTTCTGCTGCTGCTGCGGAGCATGCGCATCAATTTCTTGTGAGCTTCTG	840
Qy	1126	AGCAAAATGCTGCTTCTCAAAATGGCGAGCTCTTACCACTGTTGTTCAACTTCAAAACAG	1185
Db	841	AGCAAAATGCTGCTTCTCAAAATGGCGAGCTCTTACCACTTCTTTCACCTTTTAAACAG	900
Qy	1186	AGTTGCTGGGGCTTCAAC	1204
Db	901	AGTTGCTGGGGCTTCAAC	919
RESULT 12			
CNS09YSF			
LOCUS			
DEFINITION			
1638 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLT912E05 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi 1 (bases 1 to 1638) Castelli.V., Aury,J.M., Jaillon.O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,			
REFERENCE			
AUTHORS			

TITLE		Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 1638)
AUTHORS		Genoscope.
JOURNAL		Direct Submission
TITLE		Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT		The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_FF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES		Location/Qualifiers
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gene		
ORIGIN		Query Match 36.8%; Score 602.2; DB 3; Length 1638; Best Local Similarity 72.3%; Pred. No. 5.1e-111; Matches 797; Conservative 0; Mismatches 303; Indels 3; Gaps 1;

Qy	148	ACGACAAGAAATGCTGCTGCTGTTATAGAGGAAATGATGCTGTTCACGATCAATCA	207
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Db	382	TTGTGACTACTATTTGGTGTAGAAATGGCCAAACCAAAACAGACAATTAGCTACATGGCTG	441
Qy	268	AACGCTGTTGTTGGAACAGGATCATTCGGAATTTGATTTCCAGGCAAAATGCTTGGAAACTG	327
Db	442	AGCGTGTGTTGTTGTCACGGATCTTTTGGTGTGTTGTTCCAGGCAAAATGCTTGGACAG	501
Qy	328	GAGAATCAGTAGCCATTAAAGAGTTTTCAGAGATCCCGTTTATAAAACCCGAGAGTTGC	387
Db	502	GAGAACTGTTGCGATAAAGAAAGTTTTCAGAGATAGGAGTTACAAAGAACCGTGAGCTTC	561
Qy	388	AATTAATGCACTAATGGACCATCCAAATGTTGTTTCTTGAAGCAATGTTTCTTCTCTA	447
Db	562	AAACCATGAGGCTACTTGACCATCTCTTAATGTTGTTGTTCTGAAACCAATGTTTCTTCTCA	621
Qy	448	CAACGACTAGAGATGAGCTTCTTCTCAATCTCGTTATGGAGTATGTACCAAGACACATTTGT	507
Db	622	CCACTGAAAGAGTATGAGCTTTTACTCAATCTGTTCTTGTGATGAGTTCAGAAACTGTTT	681
Qy	508	ACCGGTTTGAAGCACTACTATAGTTTCAAAACCGAGATGCGCTATCTTCTATGTCAAC	567
Db	682	ATCGTGTATCAACACTCAACAACTGAATCAGAGAAATGCTCTTATATGCGTCAAC	741
Qy	568	TTTACATACCAAACTTTCAGAGGCTTGGCTTATATCCATATGCTCTCCCTGGTGTCTGCC	627
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QY 928 AAGAAATCGGTGCATGAACCCAACTACACAGACTTCAGATTCCCAAAATCAGAGCCC 987  
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QY 1108 TTTTCAATGAACCTCCGTAGCGCAAAAGTCTGCTTCCAAATGGCCGACCTCTACCACTG 1167  
DB 1417 TCTTGATGAGCTTCGAGATCCCTAACTACGCGCTTCCAAATGGTCTGCTTTTGGCCACCAC 1476  
QY 1168 TGTTCAACTTCAAC 1182  
DB 1477 TATTCATTTCAAGC 1491

RESULT 14  
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DEFINITION mRNA sequence.  
ACCESSION AV829186  
VERSION AV829186.1 GI:19871246  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 594)  
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,  
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.  
and Shinozaki, K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msek@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998) cDNA cleaved with BamHI  
and XhoI was ligated to modified lambda FLC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified pluescript vector. Please visit our web  
site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
details.

FEATURES  
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/clone\_lib="RAFL9"  
/notes="Site 1: BamHI; Site 2: SalI; subjected to  
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hr) treatments"  
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Best Local Similarity 99.8%; Pred. No. 8.7e-109;

Matches 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 3 GAGAGTTAGACTGTTAAAGCACATGACTTCGATACCAATCGGCGCTCCTCAGCCTCG 62  
QY 81 TCTTTAGCTCCTCAGCGCGGCATCTTACGCGGAGATCTTTGAAAAGTGTGTCCTCCGAT 140  
DB 63 TCTTTAGCTCCTCAGCGCGGCATCTTACGCGGAGATCTTTGAAAAGTGTGTCCTCCGAT 122  
QY 141 ATAGACAACGACAAGAAATGTCTGCTGTATAGAAAGAAATGATGCTGTACCGGT 200  
DB 123 ATAGACAACGACAAGAAATGTCTGCTGTATAGAAAGAAATGATGCTGTACCGGT 182  
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QY 321 GAACTGGAGAAATCAGTAGCCATTAAGAGGTTTGGCAAGATCGCGTTATAAAACCGA 380  
DB 303 GAACTGGAGAAATCAGTAGCCATTAAGAGGTTTGGCAAGATCGCGTTATAAAACCGA 362  
QY 381 GAGTTGCATTAATCGACTTAATGACCATCCAAATGTGTTTCCCTTGAAGCAATGCTTTC 440  
DB 363 GAGTTGCATTAATCGACTTAATGACCATCCAAATGTGTTTCCCTTGAAGCAATGCTTTC 422  
QY 441 TTCTCTACAACGACTAGAGATGAGTCTTCTCAATCTGTTATGAGTATGTACCAGAG 500  
DB 423 TTCTCTACAACGACTAGAGATGAGTCTTCTCAATCTGTTATGAGTATGTACCAGAG 482  
QY 501 ACATTGTACCGGTTTGAAGCACTATAGTTCAAAACAGCGGATGCTATCTTCTAT 560  
DB 483 ACATTGTACCGGTTTGAAGCACTATAGTTCAAAACAGCGGATGCTATCTTCTAT 542  
QY 561 GTCAACTTTACACATCCAAATCTTCAGAGCTTGGCTTATATCCACTACTG 612  
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RESULT 15  
LOCUS CL964803  
DEFINITION CL964803 Oryza sativa Express Library Oryza sativa (indica  
cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL964803.1 GI:52384296  
VERSION CL964803  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartioideae; Oryzaceae; Oryza.  
1 (bases 1 to 2295)  
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
Wong, G.K.S., Deng, X.W. and Wang, J.  
An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis  
Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers

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Query Match	35.4%;	Score 578.8; DB 9; Length 2295;
Best Local Similarity	75.6%;	Pred. No. 2.7e-106;
Matches 718;	Conservative 0;	Mismatches 232; Indels 0; Gaps 0;
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Qy	269	ACGTGTGTGGAACAGGATCATTCGGAATGTATTTCCAGGCAAAATGCTTGGAAACTGG 328
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Qy	329	AGAATCAGTAGCCATTAAGAAGCTTTTGCAGATCGCCGTTATAAACCAGAGAGTTGCA 388
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Qy	389	ATTAATGGACTAATGGACCATCCAAATGTGTCTTGAAGCAATGTTTCTCTCTAC 448
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Qy	449	AACGACTAGAGATGAGCTCTCCTCAATCTCGTTATGGAGTATGTACCAGAGACATTTGA 508
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Db 1002 TCTCCTTCAGTATTCGCCAAATCTGCGATGACTCGGATTCGCCAAGG 1051

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Job time : 8133.57 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 12152.4 Seconds  
(without alignment)  
6929.914 Million cell updates/sec

Title: X94939

Perfect score: 1738

Sequence: 1 AAAGAAAGAGAAAGAGAGA.....ACAAAAA 1738

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb\_ba.\*  
2: gb\_hg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1738	100.0	1738	8	ATASKRNA
2	1596.4	91.9	1670	8	AY075699
3	1565.6	90.1	1636	8	AY086529
4	1099.8	63.3	1143	6	CQ804868
5	1099.8	63.3	1143	6	AX506180
6	734.6	42.3	1636	8	ATASKDZET
7	733	42.2	1270	8	AY096698
8	733	42.2	1566	8	AY064020
9	733	42.2	1591	8	AY094423
10	732	42.1	1595	8	ATASKDNA
11	729.8	42.0	1503	8	AY087542
12	704	40.5	1572	8	AF019927
13	704	40.5	1614	8	ATASKIOTA
14	700.8	40.3	1255	8	AY051053
15	700.8	40.3	1582	8	AY035048
16	685.4	39.4	2055	8	AK073725
17	672.2	38.7	94301	8	ATF28A21
18	672.2	38.7	199075	8	ATCHRIV49
19	666	38.3	1797	8	OSKETHA

20	664.4	38.2	1825	8	AK100950
21	662.8	38.1	1818	8	AK105665
22	647.2	37.2	1744	8	BT009253
23	647	37.2	1863	8	AK102147
24	613.4	35.3	1249	8	AY142595
25	613.4	35.3	1634	8	AF428327
26	613.4	35.3	1667	8	AY046024
27	605.8	34.9	1592	8	AB059621
28	605.8	34.9	1717	8	AY085752
29	605.8	34.9	2624	8	AK099742
30	605.4	34.8	1496	8	ATASKA
31	605.4	34.8	1496	8	ATRNAASKA
32	604.8	34.8	1834	8	AY339068
33	604.2	34.8	1230	6	AX507663
34	604.2	34.8	1401	8	AY093347
35	604.2	34.8	1630	8	AY062713
36	604.2	34.8	1658	8	ATRNAASKG
37	603.8	34.7	2030	8	AY339067
38	602.6	34.7	1600	8	AK104687
39	602.6	34.7	1829	8	AK068737
40	602.6	34.7	1859	8	AY339066
41	601	34.6	1233	8	BT010466
42	601	34.6	1712	8	AY065043
43	592.6	34.1	1488	8	BT000132
44	592.6	34.1	1817	8	AY092987
45	592	34.1	2185	8	AY339065

## ALIGNMENTS

RESULT 1	ATASKRNA	1738 bp	mrna	linear	PLN 13-FEB-1998
LOCUS	ATASKRNA	A thaliana mRNA for shaggy-like kinase etha.			
DEFINITION	X94939.1	GI:1161511			
ACCESSION	ASK etha gene; shaggy-like kinase etha.				
VERSION	Arabidopsis thaliana (thale cress)				
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
ORGANISM	Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.				
REFERENCE	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)				
JOURNAL	Plant Physiol. 113, 306-306 (1997)				
REFERENCE	2 (bases 1 to 1738)				
AUTHORS	Dornelas,M.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE				
COMMENT	Corresponding genomic sequence is found in Y08947.				
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Qy	61	TCTATCTTCGGGCTTCCTTTCTCTCTCTATCGCCACAATGATCATGACCACCAAACTG	120
Dd	61	TCTATCTTCGGGCTTCCTTTCTCTCTATCGCCACAATGATCATGACCACCAAACTG	120
Qy	121	ATTGAACACTCATTTGTCCTCTCTCTCCTCAAATCCACTCTCTCTCTTTCTTTTCTCTCTC	180
Dd	121	ATTGAACACTCATTTGTCCTCTCTCTCCTCAAATCCACTCTCTCTCTTTCTTTTCTCTCTC	180
Qy	181	CTCTCTGTGCTCTATCGCCATGGCTGATGATAAGGAGATGCCGTGCTGTAGTTGATG	240
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Qy	661	ACATTCACAGTTGCCCCGGAGTTTGTTCACAGAGATCTAAAGCCCTCAAAATCTTCCTGGTTG	720
Dd	661	ACATTCACAGTTGCCCCGGAGTTTGTTCACAGAGATCTAAAGCCCTCAAAATCTTCCTGGTTG	720
Qy	721	ATCCTCTTATCTCATCAAGTCAAAATCTGTGTGATTTGGCAGTGCAGAAACAGCTCGTTAAG	780
Dd	721	ATCCTCTTACTCATCAAGTCAAAATCTGTGTGATTTGGCAGTGCAGAAACAGCTCGTTAAG	780
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	Db	901	TTCCTTCTGGTCAGCCATTATTTCCC CGGAGAAAATGCTGTGGATCAAGCTCGTGGAATAA	960
	Qy	961	TTAAAGTTCCTGGTACCAA CTCCGAGAAGAAATCCGTTGTATGAATCCCAACTACACAG	1020
	Db	961	TTAAAGTTCCTGGTACCAA CTCCGAGAAGAAATCCGTTGTATGAATCCCAACTACACAG	1020
	Qy	1021	ATTTCAAAGTTCACAGATAAAGGCCCATCCCTGGGCACAAGATCTTCCACAAAAGGATGC	1080
	Db	1021	ATTTCAAAGTTCACAGATAAAGGCCCATCCCTGGGCACAAGATCTTCCACAAAAGGATGC	1080
	Qy	1081	CCCCAGAAGCGGTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTTAAGATGCA	1140
	Db	1081	CCCCAGAAGCGGTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTTAAGATGCA	1140
	Qy	1141	CAGCGCTCGAAGCTTGTGCACATCCGTTCTTTTGAATGNACTCAGAGAACCAAAACGCTCGTT	1200
	Db	1141	CAGCGCTCGAAGCTTGTGCACATCCGTTCTTTTGAATGNACTCAGAGAACCAAAACGCTCGTT	1200
	Qy	1201	TATCAAAATGGAAGCGCTCTCCCGCCCTCTCTTCAACTTCAAAACAAGTAGTAGCTGGATCAT	1260
	Db	1201	TATCAAAATGGAAGCGCTCTCCCGCCCTCTCTTCAACTTCAAAACAAGTAGTAGCTGGATCAT	1260
	Qy	1261	CACCTGAACTGGTCAACAAGTTGATTTCCAGACCATATCAAGAGACAAATTTGGGTCTAAGCT	1320
	Db	1261	CACCTGAACTGGTCAACAAGTTGATTTCCAGACCATATCAAGAGACAAATTTGGGTCTAAGCT	1320
	Qy	1321	TCTTGAATCAATCTGGAACTTAAAGGGATCCCTGCAAAAGACAACTACTTTTTTATATAT	1380
	Db	1321	TCTTGAATCAATCTGGAACTTAAAGGGATCCCTGCAAAAGACAACTACTTTTTTATATAT	1380
	Qy	1381	AATGTACCAATTACAGAGCCACAAGGTCGPTAGTTGAAGGCAAACTGGAGGACACAATTC	1440
	Db	1381	AATGTACCAATTACAGAGCCACAAGGTCGPTAGTTGAAGGCAAACTGGAGGACACAATTC	1440
	Qy	1441	AAAGTTTTCCTCCTCAAACTCGTTCAGACAAAGCCAGCTGCTAGCAAAACCAACTACCC	1500
	Db	1441	AAAGTTTTCCTCCTCAAACTCGTTCAGACAAAGCCAGCTGCTAGCAAAACCAACTACCC	1500
	Qy	1501	AAATCTGCGAAAAACAAAACCTCCAGTGTGTATCTGCTATTTCTCTCTCTTTCAA	1560
	Db	1501	AAATCTGCGAAAAACAAAACCTCCAGTGTGTATCTGCTATTTCTCTCTCTTTCAA	1560
	Qy	1561	GTTTGTGTAAAAACACAGTCTCTCTTGTCTCAATTTCTTCTTCTTCTTCTTCTTATGTA	1620
	Db	1561	GTTTGTGTAAAAACACAGTCTCTCTTGTCTCAATTTCTTCTTCTTCTTCTTCTTATGTA	1620
	Qy	1621	AATCAGTTTGTAGTCAGAGTTTTTTTATATAGTAAAGTTTGGCAGAGAGTCAAGAAATGTA	1680
	Db	1621	AATCAGTTTGTAGTCAGAGTTTTTTTATATAGTAAAGTTTGGCAGAGAGTCAAGAAATGTA	1680
	Qy	1681	ATCAAAAGTGATATCTTTTCAACGAGGAGCTCTCTTCAAAACAAAACAAAAA	1738
	Db	1681	ATCAAAAGTGATATCTTTTCAACGAGGAGCTCTCTTCAAAACAAAACAAAAA	1738
RESULT 2				
AY075699				
LOCUS		1670 bp	mRNA	linear PLN 18-FEB-2002
DEFINITION	Arabidopsis thaliana AT4g18710/P28A21_120 mRNA, complete cds.			
ACCESSION	AY075699			
VERSION	AY075699.1			
KEYWORDS	FLI CDNA..			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			

## RESULT 2

AY075699  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AY075699 1670 bp mRNA linear PLN 18-FEB-2002  
Arabidopsis thaliana AT4g1810/F28A21\_120 mRNA, complete cds.  
AY075699  
AY075699  
AY075699.1 GI:18700187  
FLI CDNA.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Arabidopsis thaliana







Qy	509	TACAGAGAAAGACGAGCTTTTCTTGGAACTTCGGTTATGAGGATGTCCTCTGAGACGTTGTA	568
Db	481	TACAAGTAAGACGAGCTTTTCTTGGAACTTCGGTTATGAGGATGTCCTCTGAGAGCTTGTGA	540
Qy	569	TCGAGTTCTGAAACATATAGTAGTGTGCAAAACCAAGAAATGCTCTTGTCTATGTTAAACT	628
Db	541	TCGAGTTCTGAAACATATAGTAGTGTGCAAAACCAAGAAATGCTCTTGTCTATGTTAAACT	600
Qy	629	TTACAGTTTATCAGATCTTTCCGGGACATTGCTTTACATTCACAGTTGCCCCGAGTTTGTCGA	688
Db	601	TTACATGTTATCAGATCTTTCCGGGACATTGCTTTACATTCACAAATGTTGCTGGAGTTTGTCGA	660
Qy	689	CAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTCAAAATCTG	748
Db	661	CAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTCAAAATCTG	720
Qy	749	TGACTTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAACAATTTCTTTACATCTGCTC	808
Db	721	TGACTTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAACAATTTCTTTACATCTGCTC	780
Qy	809	ACGATTTCTACCGTCGACCCGAGCTCATATTTTGGTGCCACTGAGTACACAACTTCTATTGA	868
Db	781	ACGATTTCTACCGTCGACCCGAGCTCATATTTTGGTGCCACTGAGTACACAACTTCTATTGA	840
Qy	869	TATCTGGTCTGCTGGTTGTGTTCTTGTGTGAGCTTCTTCTGGTCAGGCATTAATTCGCCGG	928
Db	841	TATCTGGTCTGCTGGTTGTGTTCTTGTGTGAGCTTCTTCTGGTCAGGCATTAATTCGCCGG	900
Qy	929	AGAAAATGCTGTGATCAGCTCGTGGGAAATTAATAAGTTCTTCGGTACACCAACTCCAGA	988
Db	901	AGAAAATGCTGTGATCAGCTCGTGGGAAATTAATAAGTTCTTCGGTACACCAACTCCAGA	960
Qy	989	AGAAATCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCACAGATAAAGGCCCA	1048
Db	961	AGAAATCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCACAGATAAAGGCCCA	1020
Qy	1049	TCCCTGGCAAGAATCTTCCAAAAAGGATGCCCCAGAGCGGTGTGATTTGGCATCAAG	1108
Db	1021	TCCCTGGCAAGAATCTTCCAAAAAGGATGCCCCAGAGCGGTGTGATTTGGCATCAAG	1080
Qy	1109	GCTGCTTCAATACCTCCAGTCTTAAGTGTGACAGCGCTCGAAAGCTTTGTGCACATCCGTT	1168
Db	1081	GCTGCTTCAATACCTCCAGTCTTAAGTGTGACAGCGCTCGAAAGCTTTGTGCACATCCGTT	1140
Qy	1169	CTTTGTAGTAACCTCAGAGAAACCAACGCTCGTTTACCAATGGAGCGCTCTCCCGCCTCT	1228
Db	1141	CTTTGTAGTAACCTCAGAGAAACCAACGCTCGTTTACCAATGGAGCGCTCTCCCGCCTCT	1200
Qy	1229	CTTCAACTTCAACCAAGAGTAGCTGGATCATCACTGAACTGGTCAACAGTTGATTCC	1288
Db	1201	CTTCAACTTCAACCAAGAGTAGCTGGATCATCACTGAACTGGTCAACAGTTGATTCC	1260
Qy	1289	AGACCATATCAGAGACAAATTTGGGTCTAAGCTTCTTGAATCAATCTGGAACTTAAAGGG	1348
Db	1261	AGACCATATCAGAGACAAATTTGGGTCTAAGCTTCTTGAATCAATCTGGAACTTAAAGGG	1320
Qy	1349	ATCTGTCAAAAGACAACTACTTTTTTATATATATGTACCAATACAGAGCCCAAGGTC	1408
Db	1321	ATCTGTCAAAAGACAACTACTTTTTTATATATATGTACCAATACAGAGCCCAAGGTC	1380
Qy	1409	GTAGTTGAAGGCAAAACGTGGAGGACAAATTTCAAAGTTTTTCTCTCAAACTGTTTCAG	1468
Db	1381	GTAGTTGAAGGCAAAACGTGGAGGACAAATTTCAAAGTTTTTCTCTCAAACTGTTTCAG	1440
Qy	1469	ACAAAGCCAGCTGTAGCAAAACCAACTA-CCCAAAATCTGGGAAAAACAAAACTCTCCAG	1527
Db	1441	ACAAAGCCAGCTGTAGCAAAACCAACTA-CCCAAAATCTGGGAAAAACAAAACTCTCCAG	1500
Qy	1528	TGTTGTATCTGCTTATTTCTCTTCTCTTTTCAAGTTTGGTGAAAAACACAGTCTCTCTT	1587
Db	1501	TGTTGTATCTGCTTATTTCTCTTCTCTTTTCAAGTTTGGTGAAAAACACAGTCTCTCTT	1560
Qy	1588	TGCTTTCATTTCTCTTTCTTTTCCCCCTTAATGTAATGAGTTTGTAGTCAGAAAGTTTTTTAT	1647

Db	1561	TGCTTCATATCTTCTTCTTCTTCCCTTATGTAAATGAGTTAGTCAGAAAGTTTTTTTAT	1620
Qy	1648	ATAGTAAAGTTTGGGC	1663
Db	1621	ATAGTAAAGTTTGGGC	1636
RESULT 4			
CO804868			
LOCUS	CO804868	1143 bp	DNA
DEFINITION	Sequence 1279 from Patent WO2004035798.		linear
ACCESSION	CO804868		
VERSION	CO804868.1	GI:47111068	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 Inze, D., de Veylder, L. and Vlieghe, K.		
AUTHORS	Identification of novel e2f target genes and use thereof		
TITLE	Patent: WO 2004035798-A 1279 29-APR-2004;		
JOURNAL	Cropdesign N.V. (BE)		
FEATURES	source	Location/Qualifiers	
ORIGIN		1..1143	
	Query Match	63.3%;	Score 1099.8; DB 6; Length 1143;
	Best Local Similarity	97.6%;	Pred. No. 4.3e-271;
	Matches 1116; Conservative	0;	Mismatches 27; Indels 0; Gaps 0;
Qy	201	ATGCGCTGATGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCACCTGGT	260
Db	1	ATGCGCTGATGATAAGGAGATGCCTGCTGCTGTAGTTGATGGACATGATCAAGTCACCTGGT	60
Qy	261	CATATATTATTCACCAACATCGGTGGCAAAATGGTGACCAAAACGACAAATAGTTAC	320
Db	61	CATATATTATTCACCAACATCGGTGGCAAAATGGTGACCAAAACGACAAATAGTTAC	120
Qy	321	ATGCGGAGCGAGTTGTGTGTACAGGCTCGTTCGGGATCGTTTTCCAAAGCAAAATGTTG	380
Db	121	ATGCGGAGCGAGTTGTGTGTACAGGCTCGTTCGGGATCGTTTTCCAAAGCAAAATGTTG	180
Qy	381	GAGACTGGAGAAACCGTGGCGATAAAGAGTTTTCGAAGATAGAAGATCAAGAACCGA	440
Db	181	GAGACTGGAGAAACCGTGGCGATAAAGAGTTTTCGAAGATAGAAGATCAAGAACCGA	240
Qy	441	GAACCTCAGTTGATCGGTGTGATGATCATCCGAATGTGGTTGTTGAAGCAATGCTTC	500
Db	241	GAACCTCAGTTGATCGGTGTGATGATCATCCGAATGTGGTTGTTGAAGCAATGCTTC	300
Qy	501	TTTTTCGACTACAGAGAAGACGAGCTTTTCTCGAATCTGGTTATGGAGTATGCCCTGAG	560
Db	301	TTTTTCGACTACAGAGAAGACGAGCTTTTCTCGAATCTGGTTATGGAGTATGCCCTGAG	360
Qy	561	ACGTTGTATCGAGTTCTTGAAACATATTAGTAGTGCACAAACCAAGAAATGCCCTCTTGTCTAT	620
Db	361	ACGTTGTATCGAGTTCTTGAAACATATTAGTAGTGCACAAACCAAGAAATGCCCTCTTGTCTAT	420
Qy	621	GTTAAACTTTACAGTTATCAGATCTTCGCGGAGCTTGCTTTACATTCACAGTGGCCGGGA	680
Db	421	GTTAAACTTTACAGTTATCAGATCTTCGCGGAGCTTGCTTTACATTCACAGTGGTGTGGA	480
Qy	681	GTTTGTTCACAGAGATCTTAAGCCCTCAAAATCTTCGTTGATCCTCTTACTCATCAAGTC	740
Db	481	GTTTGTTCACAGAGATCTTAAGCCCTCAAAATCTTCGTTGATCCTCTTACTCATCAAGTC	540
Qy	741	AAAATCTGTGACTTTTGGCAGTGGCAACAGCTCGTTAAAGGTGAAACCAACATTTCTTAC	800

Db	541	AAAACTCTGTGACTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAAGCCAAACATTTCTTAC	600
Qy	801	ATCTGCTCAGGATCTTACCGTGACCGGAGCTCATATTTGGTGCCACTGAGTACAACT	860
Db	601	ATCTGCTCAGGATCTTACCGTGACCGGAGCTCATATTTGGTGCCACTGAGTACAACT	660
Qy	861	TCTATTGATATCTGGTCTGCTGGTGTGTTCTTGGCTGAGCTTCTTGGTCAAGCCATTA	920
Db	661	TCTATTGATATCTGGTCTGCTGGTGTGTTCTTGGCTGAGCTTCTTGGTCAAGCCATTA	720
Qy	921	TTCCCGGAGAAATCTGTGGATCAGCTCGTGGAATATTATAAAGTTCTTGGTACACCA	980
Db	721	TTTCCCGGAGAAATCTGTGGATCAGCTCGTGGAATATTATAAAGTTCTTGGTACACCA	780
Qy	981	ACTCGAGAGAAATCTGGTGTATGAATCCCACTACACAGATTTCAAGTTCACAGATA	1040
Db	781	ACTCGAGAGAAATCTGGTGTATGAATCCCACTACACAGATTTCAAGTTCACAGATA	840
Qy	1041	AAGGCCCATCCCTGGCACAAGATCTTCCCAAAAAGGATGCCCCAGAAGCGTTGATTG	1100
Db	841	AAGGCATCTCTGGCACAAGATCTTCCCAAAAAGGATGCCCCAGAAGCGTTGATTG	900
Qy	1101	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA	1160
Db	901	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA	960
Qy	1161	CATCCGCTCTTTCATGATCACTCAGAGAACCAAGCGCTCGTTACCAATGGAAGCGCTCTC	1220
Db	961	CATCCGCTCTTTCATGATCACTCAGAGAACCAAGCGCTCGTTACCAATGGAAGCGCTCTC	1020
Qy	1221	CCGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAAG	1280
Db	1021	CCGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAAG	1080
Qy	1281	TTGATTCAGACCATATCAAGAGCAATTTGGGTCTAAGCTTCTTGAATCAATCTGAACT	1340
Db	1081	TTGATTCAGACCATATCAAGAGCAATTTGGGTCTAAGCTTCTTGAATCAATCTGAACT	1140
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Db	1141	TAA 1143	
RESULT 5			
AX506180			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Arabidopsis thaliana (thale cress)			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.			
1			
AUTHORS			
TITLE			
JOURNAL			
The Scripps Research Institute (US) ; Syngenta Participations AG			
(CH)			
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1. 1143			
/organism="Arabidopsis thaliana"			
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Query Match 63.3%; Score 1099.8; DB 6; Length 1143;			
Best Local Similarity 97.6%; Pred. No. 4.3e-271;			
Matches 1116; Conservative 0; Mismatches 27; Indels 0; Gaps 0;			

Qy	201	ATGGCTGATGATAAGGAGATGCTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGT	260
Db	1	ATGGCTGATGATAAGGAGATGCTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGT	60
Qy	261	CATATTTATTTCCACCAATCGGTGGCAAAAATGGTGAACCAAAAAGAGATAGAGATA	320
Db	61	CATATTTATTTCCACCAATCGGTGGCAAAAATGGTGAACCAAAAAGAGATAGAGATA	120
Qy	321	ATGGCGGAGCGAGTTGGTGTACAGCTCGTTCCGAGATCGTTTCCAAAGCAAAATGTTG	380
Db	121	ATGGCGGAGCGAGTTGGTGTACAGCTCGTTCCGAGATCGTTTCCAAAGCAAAATGTTG	180
Qy	381	GAGACTGGAGAAACCGTGGCGATATAAGAGAGTTTGGCAAGATAGAGATAAAGAACCGA	440
Db	181	GAGACTGGAGAAACCGTGGCGATATAAGAGAGTTTGGCAAGATAGAGATAAAGAACCGA	240
Qy	441	GAACTTCAGTTCGATGCGTGTGATGATCATCCGAATGTGGTTTGGTGAAGCATTTGCTTC	500
Db	241	GAACTTCAGTTCGATGCGTGTGATGATCATCCGAATGTGGTTTGGTGAAGCATTTGCTTC	300
Qy	501	TTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCCTGAG	560
Db	301	TTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCCTGAG	360
Qy	561	ACGTTGTATCGAGTTCTTGAAACATTTATAGTAGTGCAGAACCAAGAAATGCTCTTGTCTAT	620
Db	361	ACGTTGTATCGAGTTCTTGAAACATTTATAGTAGTGCAGAACCAAGAAATGCTCTTGTCTAT	420
Qy	621	GTTAAACTTTTACAGTTATCAGATCTTCCGGGACCTTGTTCATTCACAGTTGCGCGGA	680
Db	421	GTTAAACTTTTACAGTTATCAGATCTTCCGGGACCTTGTTCATTCACAGTTGCGCGGA	480
Qy	681	GTTTGTACAGAGATCTAAGGCTCAAAATCTTCTGGTTGATCCTTCTTCAATCAAGTC	740
Db	481	GTTTGTACAGAGATCTAAGGCTCAAAATCTTCTGGTTGATCCTTCTTCAATCAAGTC	540
Qy	741	AAAACTCTGTGACTTTGGGAGTGCAGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC	800
Db	541	AAAACTCTGTGACTTTGGGAGTGCAGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC	600
Qy	801	ATCTGCTCAGATTTACCGTGACCCGAGCTCATATTTGGTGCCACTGAGTACACAACT	860
Db	601	ATCTGCTCAGATTTACCGTGACCCGAGCTCATATTTGGTGCCACTGAGTACACAACT	660
Qy	861	TCTATTGATATCTGGTCTGCTGGTGTGTTCTTGTGAGCTTCTTCTTGGTCAAGCCATTA	920
Db	661	TCTATTGATATCTGGTCTGCTGGTGTGTTCTTGTGAGCTTCTTCTTGGTCAAGCCATTA	720
Qy	921	TTCCCGGAGAGAAATGCTGTGGATCAGCTCGTGGAAATTTATTAAGTTCCTTGGTACACCA	980
Db	721	TTCCCGGAGAGAAATGCTGTGGATCAGCTCGTGGAAATTTATTAAGTTCCTTGGTACACCA	780
Qy	981	ACTCGAGAGAAATCCGTTGTATGAATCCCACTACACAGATTTCAAGTTCACAGATA	1040
Db	781	ACTCGAGAGAAATCCGTTGTATGAATCCCACTACACAGATTTCAAGTTCACAGATA	840
Qy	1041	AAGGCCCATCCCTGGCACAAGATCTTCCCAAAAAGGATGCCCCAGAAGCGTTGATTG	1100
Db	841	AAGGCATCTCTGGCACAAGATCTTCCCAAAAAGGATGCCCCAGAAGCGTTGATTG	900
Qy	1101	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA	1160
Db	901	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA	960
Qy	1161	CATCCGCTCTTTCATGATCACTCAGAGAACCAAGCGCTCGTTTACCAATGGAAGCGCTCTC	1220
Db	961	CATCCGCTCTTTCATGATCACTCAGAGAACCAAGCGCTCGTTTACCAATGGAAGCGCTCTC	1020
Qy	1221	CCGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAAG	1280
Db	1021	CCGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAAG	1080





Db	813	GTATTCCTCGGAGAAATCTGTGACAGCTAGTGGAGATCATAAAGTTCTTGGTAC	872
Qy	977	ACCAACTCGAGAGAAATCCGTTGTATGAATCCCACTACACAGATTTCAAGTTCCTCCACA	1036
Db	873	TCCAACTCGGAGAAATCCGTTGTATGAATCCCACTACACAGATTTCAAGTTCCTCCACA	932
Qy	1037	GATAAGGCCATCCCTGCGACAGATCTTCACAAAGGATGCCCCAGAGCGGTGA	1096
Db	933	AATCAAGCCCACTCCCTGCGACAGATCTTCACAAAGGATGCCCCAGAGCGGTGA	992
Qy	1097	TTTGGCATCAAGCGTCTTCAATCTCTCAAGTCTCAAGATCAGAGCTCGAAGCTTG	1156
Db	993	CTTGAATCTCGGCTTCTCAATCTCTCAAGTCTCAAGATCAGAGCTCGAAGCTTG	1052
Qy	1157	TGCACATCCGTTCTTGTGATGAATCAGAGAACCAACGCTCTGTTTACCAATGAGCGCC	1216
Db	1053	TGCGCATCCGTTCTTCAATGAATCCGTTGAGCAAAATGCTGCTTCCAAATGGCGACC	1112
Qy	1217	TCTCCGCTCTCTTCACTTCAATGAATCAGAGAACCAACGCTCTGTTTACCAATGAGCGCC	1276
Db	1113	TCTACACCGTTGTTTCACTTCAATGAATCAGAGAACCAACGCTCTGTTTACCAATGAGCGCC	1172
Qy	1277	CAAGTTGATTCAGACCATATCAAGAGCAATGGTCTTAAGCTTCTTGAATCAATCTGG	1336
Db	1173	CAGGTAATACAGAGCATGTGAGCGACAGATGAATGGTCTTCCATTTCAAGCTGG	1232
Qy	1337	AACTTAAAA	1345
Db	1233	ACCCTAGAA	1241
RESULT 8			
AY064020			
LOCUS			
DEFINITION	Arabidopsis thaliana putative shaggy protein kinase dzeta		
ACCESSION	AY064020.1		
VERSION	AY064020.1		
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 1566)		
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Lin, J., Miranda, M., Narusaka, M., Kawai, J., Kim, C.C., Lam, B., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis Full Length cDNA Clones		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1566)		
REFERENCE	Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C.C., Koeseema, E., Lam, B., Lin, J., Miranda, M., Narusaka, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
AUTHORS	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'). Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
COMMENT			

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koeseema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.	
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.	
Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.	
FEATURES	Location/Qualifiers
source	1..1566 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /chromosome="2" /clone="RAFL06-67-J10 (R11538)" /ecotypes="Columbia" /notes="This clone is in a modified pBluescript vector (lambda ZAP) as a XhoI/SstI insert."
gene	1..1566 /gene="At2g30980"
5'UTR	1..53 /gene="At2g30980"
CDS	54..1292 /gene="At2g30980" /codon_start=1 /evidence=experimental /product="putative shaggy protein kinase dzeta" /protein_id="AAL36376.1" /db_xref="GI:17381128" /translation="WTSIPLPQPPSLAPQPPHLLGGDSLKRPPDIDNDKEMSAVIEGNDVATGHIISTIGKNGEPKQTSYMAERVVGTGSGVGFQAKLETGSGVAIKKVLQDRYKNRELQMLRMHNVSLSKHFSTTTTRDELFLNLVMEYPTLYRLVKH YTSNQRMPIFYKLYTYQIFRGLAYIHATPGVCHRDVQNLVDPDTHOCLGDFGSAKVLVGEANISYICRYRAPELIFGATEYTSIDISWAGCVLAEILLGLPFPGE NSVDQVELIKVLGTPTRFEEIRCMNPNYDTRFQIKAHPMHVKFHKMPPEAIDLASRLIQYSPSLRCLTALBACMHPPFNELREPNARLPNRPPLPFLNFQELSGASPELINR LIPEHVRQRMQNGGPFQGP"
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ORIGIN	
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Best Local Similarity	77.4%; Pred. No. 6e-177;
Matches 889; Conservative	0; Mismatches 260; Indels 0; Gaps 0;
Qy	197 CGCATGCTGATGATAAGAGATGCTCTGCTGCTCTAGTGTGATGGACATGATCAAGTCAC 256 

Db	446	TTTCTTCTCTACACGACTAGAGTGAAGTCTTCTCTCAATCTCGTTATGGAGTATGTACC	505
Qy	557	TGAGAGTGTATCGAGTCTGAAACATATATAGTAGTGCACCAAGATGCTCTTGT	616
Db	506	AGAGACATTTGTACCGGTTTTGAAGCACTATATAGTTCAACACGCGATGCTATCTT	565
Qy	617	CTATGTTAAACTTTACAGTTATCAGATCTTCGGGAGCTTGTCTTACATTCACAGTTGGCC	676
Db	566	CTATGTCAACTTTACATACCAATCTTCAGAGCTTGGCTTATATCCATCTGCTCC	625
Qy	677	GGAGTGTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCTCTTACTCATCA	736
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Qy	737	AGTCAAAATCTGACTTTGGGAGTGGGAAACAGCTCGTTAAAGGTGAACCAACATTC	796
Db	686	GTGTAGCTCTGTGATTTTTGGAAGTGCAAAAGTACTGGTGAAGGTGAACCAACATATC	745
Qy	797	TTACATCTGCTACAGATTTCTACCGTGCACCGAGCTCATATTTGGTGGCCACTGAGTACAC	856
Db	746	ATATATCTGCTCTCGGTATTTACCGAGCTCGAAGCTCACTTTGGTGGCCAGAGATATAC	805
Qy	857	AACCTTCTATTGATATCTGGTCTCTGTTGTCTTGTCTGAGCTTCTTCTTGGTCAGCC	916
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Qy	917	ATTATTTCCCGGAGAAATGCTGTGATCAGCTCGTGGAAATTTATTAAGTCTTGGTAC	976
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Qy	1037	GATAAAGGCCATCCCTGGCACAAGATTTCTTCCAAAGAGATGCCCCGAGAGCGGTGA	1096
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Qy	1217	TCTCCCGCCTCTCTTCAACTTCAAAACAGAGTGTGGATCATCATCTGAACTGGTCAA	1276
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Qy	1277	CAAGTTGATTCAGACCATATCAAGACAAATTTGGGTCTAAGCTTCTTGAATCAATCTGG	1336
Db	1226	CAGGCTAATACAGAGCATGTGAGCGACAGATGAATGTGGGCTTTTCCATTTCAAGCTGG	1285
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Db	1286	ACCTTAGAA 1294	
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LOCUS	AY094423	Arabidopsis thaliana At2g30980/F7F1.19 mRNA, complete cds.	
DEFINITION	AY094423	Arabidopsis thaliana (thale cress)	
ACCESSION	AY094423	FLI CDNA.	
VERSION	AY094423.1	GI:20453107	
KEYWORDS	Arabidopsis thaliana		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
REFERENCE	1	(bases 1 to 1591)	

AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
TITLE	Arabidopsis cDNA clones
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1591)
AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
TITLE	Direct Submission
JOURNAL	Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length CDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
FEATURES	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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QY 917 ATTATTCCTCCGAGAGAAATGCTGCTGATCAGCTCGTGGAAATTTATTAAGTTCTTGTGAT 976
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DB 1312 ACCCTAGAA 1320

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DEFINITION A.thaliana ASK etha gene.
ACCESSION Y08947
VERSION Y08947.1 GI:1627515
KEYWORDS ASK etha gene; shaggy-like kinase etha.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Dornelas, M.C. and Kreis, M.
AUTHORS Dornelas, M.C. and Kreis, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 5985)
AUTHORS Dornelas, M.C.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1996) M.C. Dornelas, Universite de Paris Sud
(Paris XI), Institut de Biotechnologie des Plantes, Lab. Biol. du
Developpement des Plantes, Batiment 630, F-91405 Orsay Cedex,
FRANCE
COMMENT Corresponding mRNA is found in X94939.
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3380..3577)
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RESULT 11
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LOCUS Arabidopsis thaliana clone 36479 mRNA, complete sequence.
DEFINITION Arabidopsis thaliana (thale cress)
ACCESSION AY087542
VERSION AY087542.1 GI:21406280
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1503)
Haas, B.J., Volkovskiy, N., Town, C.D., Troughan, M., Alexandrov, N.,
Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
22088475
MEDLINE 12093376
PUBMED 12093376
REFERENCE 2 (bases 1 to 1503)
Brower, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1503)
Brower, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
Feldmann, K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
JOURNAL
AUTHORS
TITLE
COMMENT
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of

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this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

## FEATURES

## source

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## ORIGIN

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Matches 887; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

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RESULT 13
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DEFINITION X99696
ACCESSION X99696
VERSION 1 GI:1480077
KEYWORDS AKS iota gene; shaggy-like kinase iota.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and
Kreis,M.
Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase
Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939
and X99696) (PGR97-008)
JOURNAL Plant Physiol. 113, 306-306 (1997)
REFERENCE 2 (bases 1 to 1614)
AUTHORS Dornelas,M.C.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud
(Parixi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du
Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex,
FRANCE
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Matches 860; Conservative 0; Mismatches 260;
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RESULT 14			
LOCUS	AY051053	1255 bp mRNA linear	PLN 18-SEP-2002
DEFINITION	Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA, complete cds.		
ACCESSION	AY051053	GI:15293238	
VERSION	FLI CDNA.		
KEYWORDS	Arabidopsis thaliana (thale cress)		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsi.		
REFERENCE	1 (bases 1 to 1255)		
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etku, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, O., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis Open Reading Frame (ORF) Clones		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1255)		
	Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
COMMENT	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA': Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
	The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.		

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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Best Local Similarity	76.6%;	Pred. No.	1.1e-168;				
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QY	382	AGACTGGAGAAACCGTGGCGATAAAGAGGTTTTTCGAAGATAGAAGATACAAGAACCGAG	441				
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DEFINITION   Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA,
              complete cds.
ACCESSION   AY035048
VERSION     AY035048.1  GI:14334749
KEYWORDS    Arabidopsis thaliana (thale cress)
SOURCE      Arabidopsis thaliana
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1582)
AUTHORS     Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
              Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
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              Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
              Davis,R.W., Ecker,J.R. and Theologis,A.
              Arabidopsis Full Length cDNA Clones
              Unpublished
REFERENCE   2 (bases 1 to 1582)
AUTHORS     Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
              Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G.,
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              Arabidopsis Full Length cDNA Clones
              Unpublished

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TITLE      Direct Submission
JOURNAL     Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X.,
Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L.,
Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E.,
Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J.,
Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
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Best Local Similarity 76.6%; Pred. No. 1.1e-168;

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PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
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PR 19-MAY-1999; 99US-0134941P.  
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PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
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KW protein identification; signal transduction pathway; metabolic pathway;  
 XX promoter; termination sequence; ss.  
 OS Arabidopsis thaliana.  
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DT 18-OCT-2000 (first entry)  
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DE  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
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PN EP1033405-A2.  
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617	QY	CTATGTT	TAACCTTT	TACAGT	TATCAG	ATCTTCCG	GGACTTGT	TACATC	676
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797	QY	TTACAT	CTGCTC	ACGATTT	CTACCG	TGCACCG	CAGCTCAT	ATTTGG	856
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924	DB	TCCA	ACTCGG	GAGAAAT	TCGGT	GCATGAA	CCCCAA	ACTACAC	983
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1217	QY	TC	TCCCGC	CTCTT	CTTCA	ACTTCA	AAAGATG	AGCTG	1276
1164	DB	TCT	ACCAC	CGTGT	TTTCA	ACTTCA	AAAGATG	AGCTG	1223
1277	QY	CAAG	TGATTT	CCAG	ACCATAT	CAAG	AGACAA	ATTTGG	1336
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Db 386 CCAGAGTTGCAATTAATGCGACTAATGGACCAATCAAAATGTGGTTTCTTGAAGCATTTG 445  
Qy 497 CTTCTTTTCGACTACAGAGAAACAGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCCC 556  
Db 446 TTTCTTTCTTACAAACGACTAGAGATGAGCTTCTCTCAATCTCGTTATGGAGTATGTACC 505  
Qy 557 TGAGAGTTGTATCTGAGTTCTGAAACATATATAGTAGTGCAAAACCAAGAAATGCTCTTGT 616  
Db 506 AGAGACATTTGACCGGTTTGAAGCACTATATAGTTCAAAACGAGGATGCTATCTT 565  
Qy 617 CTATGTTAACTTTACAGTTATCAGATCTTCGGGACTTGTCTTCAATCAACAGTTGCC 676  
Db 566 CTATGTCAAACCTTTACACATACCAATCTTCAGAGGCTTGGCTTATATCAATCACTGCTCC 625  
Qy 677 GGGAGTTTGTACAGAGATCTAAGCTCAAAATCTTCTGGTTGATCTCTTACTCATCA 736  
Db 626 TGGTGTCTGCCACAGAGATGTGAACCACAAAATCTTTTGGTTGATCCCTCAACCATCA 685  
Qy 737 AGTCAAAATCTGTGACTTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAACCAAAATTC 796  
Db 686 GTGTAGCTCTGTGATTTTGAAGTGCAGAAAGTACTTGGTCAAGGTGAAGCAACATATC 745  
Qy 797 TTACATCTGTCTACAGATTTACCGTGACCCGAGCTCATATTTGGTGGCCACTGAGTAC 856  
Db 746 ATATATCTGTCTCGGTATTTACCGATCTCAGAACTCATCTTTGGTGGCCACAGATATAC 805  
Qy 857 AACTTCTATTGATATCTGGTCTGCTGGTTGTGTTCTTGTGAGCTTCTTCTTGGTCAGCC 916  
Db 806 ATCATCATTTGATATATGGTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTGGGAGCC 865  
Qy 917 ATTATTTCCCGGAGAAATCTCTGGATCAGCTCGTGGAAATTTATAAGTTCTTGGTAC 976  
Db 866 GTTATTTCCCGGAGAAATCTCTGGACCGCTAGTGGAGATCATAAAGTTCTTGGTAC 925  
Qy 977 ACCAACTCGAGAGAAATCCGTTGTATGAATCCCACTACAGATTTCAAGTTCCCA 1036  
Db 926 TCCAACCTCGGAGAAATCCGTTGCATGAACCCCAACTACACAGACTTCAGATTTCCCA 985  
Qy 1037 GATAAGGCCATCCCTGGGCACAGATCTTCCCAAAAGATGCCCCAGAGCGTTGA 1096  
Db 986 AATCAAGCCCATCCCTTGGCATAGGTTTTCCAAGCGGATGCCCTCCGGAAGCCATTGA 1045  
Qy 1097 TTTGGCATCAAGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTG 1156  
Db 1046 CTTGCATCTCGGCTTCTCAATCTCACTACCAAGTCTACGTTGACGTGCGGTCGAGGATG 1105  
Qy 1157 TGCACATCCGTTCTTTGATGAATCTAGAGAACCAAAACGCTCGTTTACCAAAATCGAGCC 1216  
Db 1106 TGGCATCCGTTTTCATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCGGACC 1165  
Qy 1217 TCTCCGCTCTCTTCAACTTCAACAGAGTAGTGGATCATCACCTGAACGTGTCAA 1276  
Db 1166 TCTACCAACCGTTGTCTCAACTTCAACAGAGTTGTCTGGGGCTTCCACCGAGCTTATCAA 1225  
Qy 1277 CAAGTTGATTTCCAGACCATATCAAGAGACAAATGGGCTTAAGCTTCTTGAATCAATCTGG 1336  
Db 1226 CAGCTTAATACAGAGCATGTGAGCGCACAGATGAATGGTGGCTTTTCCATTTCAAGCTGG 1285  
Qy 1337 AACTTAAAA 1345  
Db 1286 ACCCTAGAA 1294

RESULT 10

ACC57975  
ID ACC57975 standard; cdna; 1744 BP.

XX AC

XX ACC57975;

XX XX

DT 11-AUG-2003 (first entry)

XX XX

DE Soybean protein kinase stress-related polypeptide GmPK-3 cdna.

XX XX

KW GmPK-3; protein kinase stress-related polypeptide; PKSRP; enzyme;  
KW transgenic plant; plant; stress tolerance; drought tolerance;  
XX salt tolerance; cold tolerance; soybean; gene; ss.  
OS Glycine max.  
XX  
Key Location/Qualifiers  
FT 40.1302  
FT /\*tag= a "GmPK-3"  
FT /product= "GmPK-3"  
XX  
PN WO2003040171-A2.  
XX  
PD 15-MAY-2003.  
XX  
XX 12-NOV-2002; 2002WO-US036374.  
XX  
XX 09-NOV-2001; 2001US-0346096P.  
XX  
XX (BADI ) BASF PLANT SCI GMBH.  
XX  
XX Van Thielen N, Da Costa E SilvaO, Chen R;  
XX WPI; 2003-441522/41.  
DR P-PSDB; ABR42368.  
XX  
XX New protein kinase stress-related polypeptide coding nucleic acid, useful  
PT for producing transgenic plants with an increased tolerance to an  
PT environmental stress, e.g. high salinity, as compared to a wild type  
PT variety of the plant.  
XX  
XX Claim 1; Page 96-97; 111pp; English.  
XX  
XX The present sequence is a full-length cDNA encoding GmPK-3, a novel  
CC soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was  
CC identified on the basis of homology to Physcomitrella patens PK-3 (see  
CC ACC57962) and PK-10 (see ACC57966) sequence. GmPK-3 is an example of  
CC PKSRPs of the invention that are important for modulating a plant's  
CC response to environmental stress. Over-expression of PKSRP coding nucleic  
CC acids in a plant results in the plant's increased tolerance to  
CC environmental stress. Transgenic monocot and dicot plants are provided  
CC that show increased tolerance to high salinity, drought and low  
CC temperature  
XX  
XX Sequence 1744 BP; 502 A; 379 C; 380 G; 483 T; 0 U; 0 Other;  
SQ  
Query Match 41.7%; Score 724; DB 8; Length 1744;  
Best Local Similarity 74.8%; Pred. No. 3.9e-191;  
Matches 907; Conservative 0; Mismatches 305; Indels 0; Gaps 0;  
Qy 197 CGCCATGGCTGATGATAAGGAGATGCTGCTGTGTAGTTGATGGACATGATCAAGTCAC 256  
Db 156 CGATGTGGAGACCGATPAGGATATGTACGCTACTGTCTATTTAGGGGAATGATGCTGTAC 215  
Qy 257 TGTCTCATATTATTTCACCACCAATCGGTGGCAAAATTTGGTGAACCAAAACAGCAATTAG 316  
Db 216 TGSCCACAATAATCTCCACCACAATTTGGAGGCAAAATTTGGGAACCTTAAGAGACCATCAG 275  
Qy 317 TTACATGGCGGAGCGAGTTGTTGGTACAGGCTGTTCCGGATCGTTTCCAGCAAAATG 376  
Db 276 TTACATGGCAGAACGTTGTTGGCACTGGATCAATTTGGAGTTGTTTTCAGGCAAGTG 335  
Qy 377 TTTGGAGACTGGGAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAGATACAGAA 436  
Db 336 CTTGGAGACTGGGAAGCAGTGGCTATTAAAGGTTCTTGAACAGACAGCGGTTACAAAA 395  
Qy 437 CCAGAACTTTCAGTTGATCGTGTGATGATCATCCGAATGTGGTTTGTGTGAAGCATTC 496  
Db 396 TCGTGAATTGCACTTAATGCGCTTAATGGATCACCCCTAATGTAATTTCCCTGAAGCACTG 455  
Qy 497 CTTCTTTTTCGACTACAGAGAAACAGAGCTTTTCTTGAACCTGTTTATGGAGTATGTCCC 556  
Db 456 TTTCTTTCTCCACAACAGCAGAGATGAACCTTTTCTAAACTTGGTAATGGAATATGTTC 515



PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140918P.	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157533P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144334P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159329P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159331P.
PR	21-JUL-1999;	99US-0144814P.	PR	14-OCT-1999;	99US-0159332P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145919P.	PR	25-OCT-1999;	99US-0161406P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161359P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161992P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.	Query Match 40.6%; Score 705.6; DB 3; Length 1567;		
PR	05-AUG-1999;	99US-0147260P.	Best Local Similarity 76.9%; Pred. No. 5.le-186;		
PR	06-AUG-1999;	99US-0147303P.	Matches 861; Conservative 0; Mismatches 259; Indels 0; Gaps 0;		
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148565P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149175P.			
PR	18-AUG-1999;	99US-0149426P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149829P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150884P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	27-AUG-1999;	99US-0151080P.			
PR	30-AUG-1999;	99US-0151303P.			
PR	31-AUG-1999;	99US-0151438P.			
PR	01-SEP-1999;	99US-0151930P.			
QY	202	TGCGTATGATGAAGGAGATCGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTC	261	202	TGCGTATGATGAAGGAGATCGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTC
DB	135	TGGAATCTGATGAAGAAATGCTGACGCTGTTATTGAGGAATGACGCTGTTACTGGTC	194	135	TGGAATCTGATGAAGAAATGCTGACGCTGTTATTGAGGAATGACGCTGTTACTGGTC
QY	262	ATATTATTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAGACAATAGTTACA	321	262	ATATTATTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAGACAATAGTTACA
DB	195	ATATCATTTCCACTACTATAGGAGGCAAAACGGCGAACCAAGCAGACCATAGTTACA	254	195	ATATCATTTCCACTACTATAGGAGGCAAAACGGCGAACCAAGCAGACCATAGTTACA
QY	322	TGCGGAGCGAGTGTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAGCAAAATGTTGG	381	322	TGCGGAGCGAGTGTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAGCAAAATGTTGG
DB	255	TGCGTGAAGCGGTTGTTGGAACAGGTTTCATTCGGGATGTTGTTTCAGGCGAAATGCTGG	314	255	TGCGTGAAGCGGTTGTTGGAACAGGTTTCATTCGGGATGTTGTTTCAGGCGAAATGCTGG
QY	382	AGACTCGAGAACCGTGGCGATAAAGAGTTTTCAGATAGCAAGATACAAGAACCGAG	441	382	AGACTCGAGAACCGTGGCGATAAAGAGTTTTCAGATAGCAAGATACAAGAACCGAG
DB	315	AACTGGGAATCAGTAGCCATTAAAGGCTTTGCAAGATCGACGCTATAAACCGTG	374	315	AACTGGGAATCAGTAGCCATTAAAGGCTTTGCAAGATCGACGCTATAAACCGTG
QY	442	AACTTCAGTTGCGTGTGATCGATCATCCGAATGTTGTTTGAAGCATTGCTTCT	501	442	AACTTCAGTTGCGTGTGATCGATCATCCGAATGTTGTTTGAAGCATTGCTTCT
DB	375	AGTTGCAACTAATCGACCAATGATCACCCTGCTCTCTCTGGAAGCCTGTTCT	434	375	AGTTGCAACTAATCGACCAATGATCACCCTGCTCTCTCTGGAAGCCTGTTCT
QY	502	TTTCGACTACAGAAAGACGAGCTTTCTTGAACTTGGTATGAGGATGTCCTCGGAGA	561	502	TTTCGACTACAGAAAGACGAGCTTTCTTGAACTTGGTATGAGGATGTCCTCGGAGA
DB	435	TCTCTACAACGAGTAGAGCTCTCTCTCAACCTTGTATTGGAGTATGTACCTGAGA	494	435	TCTCTACAACGAGTAGAGCTCTCTCTCAACCTTGTATTGGAGTATGTACCTGAGA





PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.	QY	223	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	282
PR	09-JUL-1999;	99US-0142320P.	PR	28-SEP-1999;	99US-0156458P.	PR	228	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	287
PR	12-JUL-1999;	99US-0142377P.	PR	29-SEP-1999;	99US-0156596P.	PR	343	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	402
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.	PR	348	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	407
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157533P.	PR	463	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	522
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.	PR	408	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	467
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.	PR	523	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	582
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.	PR	468	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	527
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.	PR	583	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	642
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.	PR	528	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	587
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.	PR	643	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	702
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.	PR	588	CTGCTGCTAGTGTGATGGACATGATCAAGTCACTGGTCACTATTAATTTCCACCACAATCG	647
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.	PR			
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.	PR			
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.	PR			
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.	PR			
PR	20-JUL-1999;	99US-0144633P.	PR	14-OCT-1999;	99US-0159638P.	PR			
PR	21-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159584P.	PR			
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-0160741P.	PR			
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160767P.	PR			
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.	PR			
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.	PR			
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.	PR			
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.	PR			
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.	PR			
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.	PR			
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.	PR			
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.	PR			
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.	PR			
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.	PR			
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.	PR			
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.	PR			
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161361P.	PR			
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161362P.	PR			
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.	PR			
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161922P.	PR			
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.	PR			
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.	PR			
PR	04-AUG-1999;	99US-0147302P.	PR			PR			
PR	05-AUG-1999;	99US-0147192P.	PR			PR			
PR	05-AUG-1999;	99US-0147260P.	PR			PR			
PR	06-AUG-1999;	99US-0147303P.	PR			PR			
PR	06-AUG-1999;	99US-0147303P.	PR			PR			
PR	08-AUG-1999;	99US-0147493P.	PR			PR			
PR	08-AUG-1999;	99US-0147493P.	PR			PR			
PR	10-AUG-1999;	99US-0148171P.	PR			PR			
PR	11-AUG-1999;	99US-0148319P.	PR			PR			
PR	12-AUG-1999;	99US-0148341P.	PR			PR			
PR	13-AUG-1999;	99US-0148565P.	PR			PR			
PR	13-AUG-1999;	99US-0148684P.	PR			PR			
PR	16-AUG-1999;	99US-0149368P.	PR			PR			
PR	17-AUG-1999;	99US-0149175P.	PR			PR			
PR	18-AUG-1999;	99US-0149426P.	PR			PR			
PR	20-AUG-1999;	99US-0149722P.	PR			PR			
PR	20-AUG-1999;	99US-0149723P.	PR			PR			
PR	20-AUG-1999;	99US-0149929P.	PR			PR			
PR	23-AUG-1999;	99US-0149302P.	PR			PR			
PR	23-AUG-1999;	99US-0149303P.	PR			PR			
PR	25-AUG-1999;	99US-0150566P.	PR			PR			
PR	25-AUG-1999;	99US-0150884P.	PR			PR			
PR	27-AUG-1999;	99US-0151065P.	PR			PR			
PR	27-AUG-1999;	99US-0151066P.	PR			PR			
PR	27-AUG-1999;	99US-0151080P.	PR			PR			
PR	30-AUG-1999;	99US-0151303P.	PR			PR			
PR	31-AUG-1999;	99US-0151438P.	PR			PR			
PR	01-SEP-1999;	99US-0151930P.	PR			PR			
PR	07-SEP-1999;	99US-0152363P.	PR			PR			
PR	10-SEP-1999;	99US-0153070P.	PR			PR			
PR	13-SEP-1999;	99US-0153758P.	PR			PR			
PR	15-SEP-1999;	99US-0154018P.	PR			PR			
PR	16-SEP-1999;	99US-0154039P.	PR			PR			
PR	20-SEP-1999;	99US-0154779P.	PR			PR			
PR	22-SEP-1999;	99US-0155139P.	PR			PR			
PR	23-SEP-1999;	99US-0155486P.	PR			PR			

Query Match 38.9%; Score 676.8; DB 3; Length 1653;

Best Local Similarity 75.3%; Pred. No. 5.8e-178;

Matches 843; Conservative 0; Mismatches 277; Indels 0; Gaps 0;





QY 957 ATTATTAAGTTCTTGGTACACCACTCAGAGAAATCCGTTGTATGATCCCAACTAC 1016  
 DB 869 ATTATCAAGGTTCTTGGTACTCCAAACCCGTTGAGGAAATTCGGTGCATGAACCCCAACTAT 928  
 QY 1017 ACAGATTTCAAGTCTCCACAGATAAAGGCCATCCCTGGCACAAGATCTTCCACAAAAGG 1076  
 DB 929 ACCGAGTTCAAGTCTCCACAGATAAAGGCCATCCCTGGCACAAGATCTTCCACAAAAGG 988  
 QY 1077 ATGCCCCAGAGCGGTTGATTGGCATCAAGGCTGCTTCAATCTCTCCAAAGTCTAAGA 1136  
 DB 989 ATGCCCGCTGAAGCTATAGATCTGCTCCGCCCTTCCAGTATTCACCAATCTACGT 1048  
 QY 1137 TGCACAGCGCTCAGCTGTGTCATCGTCTTGTGATGAATCAGAGAACCAACGCT 1196  
 DB 1049 TGCATGCTCTTGATGTCATGTCATCTTCTTTGATGAGCTACGTGAGCCGAATGCA 1108  
 QY 1197 CTTTTACCAAAATGGAGCGGCTCTCCCGCTCTCTTCAACTTCAAAACAAAGATAGCTGA 1256  
 DB 1109 CCGTTGCCGAATGGCGGCCCATCTCTCTCTGTTCAACTTCAAAACCAAGATAGCTGA 1168  
 QY 1257 TCATCAGCTGAAGTGGTCAACAAAGTTGATTCAGAGACCATATCAAGAGACAAATGGGTCTA 1316  
 DB 1169 GCCTCTCCAGAGCTCATCAACAGGCTTGTTCGGAACATGTTCCGAGCGCAAAATGGCCCC 1228  
 QY 1317 AGCTTC 1322  
 DB 1229 AACTTC 1234

RESULT 15  
 ABQ82534  
 ID ABQ82534 standard; cDNA; 1673 BP.  
 AC ABQ82534;  
 DT 19-DEC-2002 (first entry)  
 DE Wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15.  
 KW Glycogen synthase kinase; kinase; enzyme; plant; immunological screening;  
 KW plant breeding; gene; ss.  
 OS Triticum aestivum.  
 FH Key Location/Qualifiers  
 FT 44..1252  
 FT /\*tag= a  
 FT /product= "glycogen synthase kinase"  
 PN US2002120949-A1.  
 XX 29-AUG-2002.  
 XX 14-MAY-2001; 2001US-00854731.  
 XX 10-JUL-1998; 98US-0092438P.  
 PR 02-JUL-1999; 99US-00347801.  
 XX (ALIE/) ALLEN S M.  
 XX Allen SM;  
 XX WPI; 2002-731384/79.  
 DR P-PSDB; ABP53636.  
 XX New calcium-dependent phosphorylase kinase and glycogen synthase kinase  
 PT polypeptides, for altering level of expression of kinase polypeptides in  
 PT plants.  
 XX Claim 15; Page 22-24; 41pp; English.  
 PS The present invention describes kinase polypeptides (I) such as a calcium

-dependent phosphorylase kinase polypeptide comprising a sequence of 101,  
 623, 137 or 111 (see ABP53629 to ABP53632) amino acids, and a glycogen  
 synthase kinase polypeptide comprising all or a portion of a sequence of  
 410, 105, 399 or 402 (see ABP53633 to ABP53636) amino acids. (I) is  
 useful for immunological screening of cDNA expression libraries, and for  
 preparing antibodies against the polypeptides, where the antibodies would  
 be useful for detecting (I) in situ or in vitro, in cell extracts.  
 Nucleic acids (II) encoding (I) can be used to isolate cDNAs and genes  
 encoding homologous proteins from the same or other plant species. (II)  
 can also be used for creating transgenic plants in which (I) is present  
 at higher or lower levels than normal or in cell types or in  
 developmental stages in which they are not normally found. (II) are  
 useful as probes or primers. The polynucleotides may be used as probes  
 for genetically and physically mapping the genes that they are a part of  
 and used as markers for traits linked to those genes. The information can  
 be used in plant breeding in order to develop lines with desired  
 phenotypes. The present sequence encodes a glycogen synthase kinase from  
 the present invention

XX SQ Sequence 1673 BP; 419 A; 421 C; 408 G; 424 T; 0 U; 1 Other;  
 Query Match 37.4%; Score 649.2; DB 6; Length 1673;  
 Beat Local Similarity 74.9%; Pred. No. 3e-170;  
 Matches 813; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 237 GATGGACATGATCAAGTCACTGGTCAATATTTTCCACCAATCGTGGCAAAATGTT 296  
 DB 149 GAGGGAAACGACCGCATGACCGGTCAATCATCTCCACACCATCGCGGCAAGAACGCG 208  
 QY 297 GAACCAACACAGACAATAGTTACATGGCGGAGCGAGTTGTGTACAGGCTCGTTCGGG 356  
 DB 209 GAGCCCAAGCAGACGATTAGCTACATGGCGGAGCGGTTGTGGGCACTGTTTCGTTTGGC 268  
 QY 357 ATCGTTTTCCAAAGCAAAATGTTTGGAGACTGCGAGAAACCGTGGCGCATAAAGAGGTTTG 416  
 DB 269 ATCGTCTTTTCCAGGCTAATGCTCGAACCAGCGGAGATGTTGGGCAATTAAGAGGTA 328  
 QY 417 CAAGTAGAAGATCAAGAACCGAGAACTTCAGTTGATGCGTGTGATGATGATATCCGAAT 476  
 DB 329 CAGGACAGACGCTACAGAACCGTGCAGCTTATGCGTTCGATGATCATTCATTCAT 388  
 QY 477 GTGGTTGTTTGAAGCATTGCTCTTTTCGACTCAGAGAAAGACGAGCTTTCTTGGAC 536  
 DB 389 GTTGTCTCCCTCAAGCACTGCTCTTCTCAACCAACAGTAGAGATGAGTGTCTCTGAC 448  
 QY 537 TTGTTATGAGTATGTCCTTGAGACGTTGTATCGAGTTCTGAAACATATAGTAGTGA 596  
 DB 449 CTTGTGATGAGTATGTCCTCGGAGACGCTATACCGGCTGCTTACGACTACAGTATGCC 508  
 QY 597 AACCAAGAATGCCTCTTGTCTATGTTAAATTTTACAGTTATCAGATCTTCGGGAGCTT 656  
 DB 509 AACCAAGGAGTGCCTTATCTATGTCAAGCTTTTACATGATATCAGCTTTTACAGGGGCTA 568  
 QY 657 GCTTACATTACAGTGGCCGGGAGTTTGTACAGAGATCTAAGCCTCAAAATCTTCTG 716  
 DB 569 GCTTATGTTTCACTGTTTCCAGGAGTTTGGCCACAGGAGTGTGAACCAAAATGTTTGG 628  
 QY 717 GTTGATCTCTTACTCAAGTCAAAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTT 776  
 DB 629 GTTGATCTCTTAAACCATCAAGTCAAGTCTGTGACTTTGGAGTGCAGAAAGTCTTGTA 688  
 QY 777 AAAGTGAACCAAAATTTTACATCTGCTCAGGATTTCTACCGTGCACCCGAGCTCAT 836  
 DB 689 CCGTGTGAACCAACATAGCATACATATGCTCTGCTACTATCGTCTCTCGAGCTCAT 748  
 QY 837 TTTGGTGCATGAGTACAGAACTTCTATGATATCTGCTGCTGCTGTTGTTCTTCTGCT 896  
 DB 749 TTTGGTGAACGAATATACAACTTCAATAGACATATGCTCAGCTGAGTGTGTTCTTGA 808  
 QY 897 GAGCTTCTTCTTGGTCAAGCAATTTATCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAA 956  
 DB 809 GAGCTACTTCTTGGTCAAGCACTTCTGTTTCCAGGAGAGACTGCGGTTGATCAGCTAGTGG 868

QY	957	ATTATTAAGTTCTTGGTACCACTCGAGAAGAAATCCGTTGTATGAATCCCAACTAC	1016
Db	869	ATTATCAAGTTCTTGGTACTCAACCCGTTAGGAAATTCGGTGCATGAACCCCACTAT	928
QY	1017	ACAGATTTCAAGTTCCCAAGATAAAGGCCATCCCTGGCACAAGATCTTCCACAAAAGG	1076
Db	929	ACCGAGTTCAAGTTTCTCAGATTAAAGGCTCATCTTGGCACAAGATTTTCCACAGAGA	988
QY	1077	ATGCCCCCAGAGCGGTTGATTTGGCATCAAGGCTGTTCAATACTCTCCAAGTCTAAGA	1136
Db	989	ATGCCCGCTGAAGCTATAGATCTTGCTCCCGCTTCTCCAGTATTCACCAATCTACGT	1048
QY	1137	TGCACAGCGTCCGAAGCTTGTGCACATCCGTTCTTTGATGAATCAGAGAACCACAAACGCT	1196
Db	1049	TGCACGTCTCTTGATGCATGTGCACATTCCTTCTTTGATGAGCTACGTGAGCGGAATGCA	1108
QY	1197	CGTTTACCAAAATGGAGCGGCTCTCCCGCTCTCTTCAACTTCAACAAGAAGTAGCTGGA	1256
Db	1109	CGTTTCCGAAATGGCGGCCCATTCCTCTCTGTTCAACTTCAAACTGAACCTAGCGAAC	1168
QY	1257	TCATCACCTGAACCTGGTCAACAAAGTTGATTCAGAGCCATATCAAGAGACAAATGGGTCTA	1316
Db	1169	GCCTCTCCAGAGCTCATCAACAGGCTTGTTCCGGAACATGTTGACGCGCAAAATGSCCCC	1228
QY	1317	AGCTTC	1322
Db	1229	AACTTC	1234

Search completed: June 23, 2005, 11:47:02  
Job time : 1367.08 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	734.6	42.3	1636	4	US-09-578-194-6	Sequence 6, Appli
2	649.2	37.4	1673	3	US-09-347-801-15	Sequence 15, Appl
3	649.2	37.4	1673	4	US-09-854-731-15	Sequence 15, Appl
4	590	33.9	1814	3	US-09-347-801-9	Sequence 9, Appli
5	590	33.9	1814	4	US-09-854-731-9	Sequence 9, Appli
6	530.4	30.5	1429	3	US-09-347-801-13	Sequence 13, Appl
7	530.4	30.5	1429	4	US-09-854-731-13	Sequence 13, Appl
8	399.6	23.0	1952	4	US-09-566-921-24	Sequence 24, Appl
9	399.6	23.0	2154	3	US-09-488-856A-3	Sequence 3, Appli
10	393.2	22.6	2088	2	US-08-602-264A-1	Sequence 1, Appli
11	393.2	22.6	2088	3	US-08-461-018A-1	Sequence 1, Appli
12	393.2	22.6	2088	3	US-09-216-958-1	Sequence 1, Appli
13	391.6	22.5	1389	3	US-09-489-765A-3	Sequence 3, Appli
14	391.6	22.5	1389	4	US-09-016-434-1414	Sequence 1414, Ap
15	391	22.5	1972	2	US-08-602-264A-2	Sequence 2, Appli
16	391	22.5	1972	3	US-08-461-018A-2	Sequence 2, Appli
17	391	22.5	1972	3	US-09-216-958-2	Sequence 2, Appli
18	286.4	16.5	1185	4	US-09-248-796A-4396	Sequence 4396, Ap
19	163	9.4	304	4	US-09-313-294A-6825	Sequence 6825, Ap
20	142.4	8.2	305	4	US-09-313-294A-5874	Sequence 5874, Ap
21	142.2	8.2	286	4	US-09-313-294A-2895	Sequence 2895, Ap
22	129.8	7.5	1236	4	US-09-248-796A-4397	Sequence 4397, Ap
23	115.6	6.7	372	4	US-09-313-294A-6721	Sequence 6721, Ap
24	107	6.2	584	3	US-09-347-801-11	Sequence 11, Appl
25	107	6.2	584	4	US-09-854-731-11	Sequence 11, Appl
26	106.4	6.1	275	2	US-09-313-294A-1703	Sequence 1703, Ap
27	101	5.8	479	2	US-08-602-264A-13	Sequence 13, Appl

317	Qy	TTATCATGCGCGAGCGAGTTGTTGGTATCAGGCTCGTTTCGGGATCGTTTTCCAGCAAAATG	376
257	Db	TTATCATGCGCGAAACGTCGTGTTGTGAACAGGATCATATCCGAAATGTGTATTTCCAGGCAAAATG	316
377	Qy	TTTGGAGACTGGAGAAACCGTGGCGGATAAAGAAGGTTTTGCAAGATAGAAGATACAAGAA	436
317	Db	CTTGGAACCTGGAGANCTAGTAGCCATTTAGAAGGTTTTGCAAGATCGCGTTATAAANA	376
437	Qy	CCGAGAACTTCAAGTTGATGCGTGTGATGGATCAATCCGAATGTGTGTTGTTGAAGCAATG	496
377	Db	CCGAGAGTTGCAATTAATGCGACTAAATGGACCATCCAAATGTGTGTTTCCTTGAAGCAATG	436
497	Qy	CTTCTTTTTGCACTACAGAGAAAGACGAGCTTTTCTTGAACTTGTTGATGAGATATGTCCTC	556
437	Db	TTTTCTTCTCTACAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATATGTACC	496
557	Qy	TGAGACGTTGTATCGAGTTCTGAAACATTAAGTAGTGCAAAACCAAAAGAAATGCTCTTGT	616
497	Db	AGACACATTTGACCGGTTTTGAAGCACTATACTAGTTTCAAAACGACGGATGCTATCTTT	556
617	Qy	CTATGTTAAACTTTACAGTTATCAGATCTTCCCGGGGACTTGCTTTACATTCACAGTTGCCCT	676
557	Db	CTATGTCAAACTTTTACACATACCAAACTCTTCAGAGGCTTGCTTTATATCATCTACTGCTCC	616
677	Qy	GGGAGTTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCA	736
617	Db	TGGTGTCTGCCACAGAGATATAAAACACAAATCTTTTGGTTGATCCCAACCCATCA	676
737	Qy	AGTCAAAATCTGTCACTTTGGCAGTCGGAACAGCTCGTTAAAGGTGAACCAAACTTTC	796
677	Db	GTGTAAAGCTCTGTATTTTGAAGTGCAAAAGTACTGGTGAAGGTGAACCAAAACATATC	736
797	Qy	TTACATCTGCTCAGATTTCTACGTCGACCGGAGCTCATATTTGGTGCCTCAGTACAC	856
737	Db	ATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATAC	796
857	Qy	AACTTCTATTGATATCTGGTCTGCTGGTTGTGTTCTTGTCTGAGCTTCTTTTGGTCAAGCC	916
797	Db	ATCATCCATTGATATATGGTCTGCTGGTTGTGTTCTGCGAGAGCTACTTCTTGGCGAGCC	856
917	Qy	ATTATTTCCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATTAATTAAGTTCTTTGGTAC	976
857	Db	GTTATTTCCCGGGAGAAATTTCTGTGGACCAAGCTAGTGGAGATCAATAAGGTTCTTTGGTAC	916
977	Qy	ACCAACTCGAGAAGAAATCCGTTCTGATGAATCCCAACTACACAGATTTCAAGTTTCCCA	1036
917	Db	TCCAACCTCGCGAAGAAATCCGGTGCATGAACCCAAATCTACAGACTTCAGATTTCCCA	976
1037	Qy	GATAAAGGCCCATCCCTGGCAACAAGATCTTCCACAAAGGATGCCCCAGAGCGGTGA	1096
977	Db	AATCAAAAGCCCCACCTTTGGCATAAGGTTTTCCACAAGCGGATGCTCCGGAAGCCAATGA	1036
1097	Qy	TTTTGGCATCAAGGCTGCTCAATACTCTCAAGCTTAAGATGCACAGGCTCGAAGCTTG	1156
1037	Db	CTTTGGCATCTCGGCTTCTTCAATACTCACCAAGCTACAGTTGCACTGCGCTCGAGGGATG	1096
1157	Qy	TGCACTCCGTTCTTTGATGAACCTCAGAGAACCAACGCTCGTTTACAAATGACGCGCC	1216
1097	Db	TGCGCATCCGTTTTTCAATGAACCTCCGTGAGCCAAATGCTCGTCTTCCAAATGSCCGACC	1156
1217	Qy	TCTCCGGCTCTCTTCAACTTTCAAAACAAGAAGTAGCTGGATCATCACTGAACTGGTCAA	1276
1157	Db	TCTACCACCGTGTGTCAACTTTCAACACAAGAGTTGTCTTGGGGCTTTACCGGAGCTTATCAA	1216
1277	Qy	CAAGTTGATTCCAGACCATATCAAGAGACAAATTTGGGCTTAAGCTTCTTGAATCAATCTGG	1336
1217	Db	CAGCTAATACAGAGCATGTGCGGCACAGATGAATGGTGGCTTTCATTTCAAGCTGG	1276
1337	Qy	AACTTAAAA	1345
1277	Db	ACCCTAGAA	1285



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QY 897 GAGCTTCTTCTTGGTCAAGCATTATTTCCCGGAGAAATGCTGTGATCAGCTCTCGTGA 956
DB 809 GAGCTACTTCTTGGTCAAGCCTCTGTTTCCAGAGAGACTGCGGTGTATCAGCTAGTGGAG 868
QY 957 ATTATTAAGTTCTTGGTACACCAACTCCGAGAGAAATCCGTTGTATGAATCCCAACTAC 1016
DB 869 ATTATCAAGTTCTTGGTACTCCAAACCGTGAGGAAATTCGGTGCATGAACCCCAACTAT 928
QY 1017 ACAGATTTCAAGTTCCCAAGATAAGGCCATCCCTGGCAAGATCTTCCACAAAAGG 1076
DB 929 ACCGAGTTCAAGTTCTTCCAGATTAAGGCTCATCTCTGGCAAGATTTTCCACAAAGAG 988
QY 1077 ATGCCCCCAAGAGCGTTGATTTGGCATCAAGCGTCTTCAATATCTTCCAGTCTTAAGA 1136
DB 989 ATGCCCGCTGAAGCTATAGATCTTCCCTCCCGCTTCTCCAGTATTCACCAATCTAGCT 1048
QY 1137 TGCACAGCGCTCGAAGCTTGTGCATATCGTTTCTTGTGATGAATCCAGAAACCAACGCT 1196
DB 1049 TGCACGTCTTGTATGATGTCACATTCCTTCTTGTGATGAGCTACGTGAGCCGATGCA 1108
QY 1197 CGTTTACCAATGAGAGCGCTCTCCGGCTCTCTTCAACTTCAAAACAAGAGTAGCTGGA 1256
DB 1109 CGCTTGCAGAAATGGCGGCCATTTCCCTCTCTGTTCAACTTCAAAACCTGAACCTAGCGA 1168
QY 1257 TCATCAGCTGAAGCTGTCACAAAGTTGATTCAGACCATATCAAGAGCAATTTGGGTCTA 1316
DB 1169 GCCTCTCCAGAGCTCATCAACAGGCTTGTTCGGGAACATGTTTCGACGGCAAAATGGCCCC 1228
QY 1317 AGCTTC 1322
DB 1229 AACTTC 1234

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RESULT 3

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US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-854-731-15

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Query Match 37.4%; Score 649.2; DB 4; Length 1673;
Best Local Similarity 74.9%; Pred No. 2,4e-175;
Matches 813; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 237 GATGACATGATCAAGTCACTGGTCAATATTTCCACCAATCGGTGGCAAAATGGT 296
DB 149 GAGGGAACGACGCCATGACCGGTCACTATCTCCACCACCATCGCGGCAAGAACGGC 208
QY 297 GAACCAAAACAGACAAATAGTTAGTATGCGGAGCGAGTTGGTACAGGCTCGTTCGG 356
DB 209 GAGCCCAAGCAGACATAGCTACATGCGGAGCGCGTTGTGGCACTGGTTCTGTTTGGC 268
QY 357 ATCGTTTTCCAGCAAAATGTTTGGAGACTGGAGAAACCGTGGCGCATAAAGAGGTTTG 416
DB 269 ATCGTCTTTCAGGCTAAATGCTTGGAAACCGGGGAGATGTTGGGCAATTAAGAGGTACTG 328

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QY 417 CAAGATAGAGATCAAGAACCGAGAACTTTCAGTTGATGCGTGTGATGATCATCGGAT 476
DB 329 CAGGACAGACGGTCAAGAACCGTGAGCTTATGCGTTTCGATGATCATTCATTCAT 388
QY 477 GTGGTTCTTCTTGAAGCATTTGCTTCTTTCGACTACAGAGAAAGAGAGCTTCTTCTGAAC 536
DB 389 GTTGTCTCCCTCAAGCACTGCTTCTTCTCAACCAAGTAGAGATGAGCTGTCTCTGAAC 448
QY 537 TTGGTATGAGATGATGCTCCCTGAGACGTTGTATCGAGTTCTGAAAACATTTATAGTAGTGA 596
DB 449 CTTGTATGAGATGATGCTCCCGAGAGCGCTATACCGCGTGTCTTAAGCACTACAGTAATGCC 508
QY 597 AACCAAGAAATGCCCTTGTCTATGTTTAACTTTTACAGTTATCAGATCTTCCGGGACTT 556
DB 509 AACCAAGGGAATGCCGCTTATCTATGTCAGGCTTTTACATGTATCAGCTTTTATAGAGGCT 568
QY 657 GCTTACATTTACAGTTGCGCGGAGTTTGTTCACAGAGATCTAAAGCCTCAAAATCTTCTG 716
DB 569 GCTTATGTTTCACTATGTTTCCAGGAGTTTGCACAGGATGTGAAACCAACAAATGTTTGG 628
QY 717 GTTGTATCTTCTTACATCAAGTCAAAATCTGTGACTTTGGCAGTGCAGAAACAGCTCGTT 776
DB 629 GTTGTATCTCTTAAACCACTCAAGTCAAGATCTGTGACTTTGGAAGTGCAAAAGTTCTGG 688
QY 777 AAAGTGAACCAACAAATTTCTTACATCTGCTCAAGTTCTACCGTGCACCGGAGCTCAT 836
DB 689 CTTGTGAACCAACCAATAGCATATATGCTCTCGTACTATCTGCTCTCTGAGCTCAT 748
QY 837 TTTGTGTCACATGAGTACACAACTTCTATGATATCTGCTCTGCTGTTGTTGTTCTTGTCT 896
DB 749 TTTGTGCACTGAATATACAACTTCAATAGACATATGCTGAGTGTGATGTTGTTCTTGTGA 808
QY 897 GAGCTTCTTCTTGGTCAAGCAATTTATCCCGGAGAAAAATGCTGTGGATCAGCTCGTGGAA 956
DB 809 GAGCTACTTCTTGGTCAAGCTCTGTTTCCAGAGAGACTGCGGTTGTATCAGCTAGTGGAG 868
QY 957 ATTATTAAGTTCTTGGTACACCAACTCGAGAGAAATCCGTTGTATGATGATTCGCAACTAC 1016
DB 869 ATTATCAAGTTCTTGGTACTCCAAACCGTGAGGAAATTCGGTGCATGAACCCCAACTAT 928
QY 1017 ACAGATTTCAAGTTTCCCAAGATAAGGCCCATCCCTGGCAAGATCTTCCACAAAAGG 1076
DB 929 ACCGAGTTCAAGTTTCTTCAAGTTAAGCTCATCTTGGCAAGATTTTCCACAAAGAG 988
QY 1077 ATGCCCCCAAGAGCGTTGATTTGGCATCAAGGCTGCTTCAATATCTTCCAGTCTTAAGA 1136
DB 989 ATGCCCGCTGAAGCTATAGATCTTGGCTCCCGCTTCTCCAGTATTTCAACCAATCTAGCT 1048
QY 1137 TGCACAGCGCTCGAAGCTGTTGTGCATCTCGTTCTTGTATGAATCAGAGAACCAACGCT 1196
DB 1049 TGCACGTCTTGTATGATGTCACATTTCTTCTTGTATGAGTACGTGAGCCGATGCA 1108
QY 1197 CGTTTACCAATGAGAGCGCTCTCCCGCTCTTCAACTTCAAAACAAGAGTAGCTGGA 1256
DB 1109 CGTTTGCAGAAATGGCGGCCATTTCCCTCTCTGTTCAACTTCAAAACCTGAACCTAGCGA 1168
QY 1257 TCATCAGCTGAAGCTGTCACAAAGTTGATTCAGACCATATCAAGAGCAATTTGGGTCTA 1316
DB 1169 GCCTCTCCAGAGCTCATCAACAGGCTTGTTCGGGACATGTTTCGACGGCAAAATGGCCCC 1228
QY 1317 AGCTTC 1322
DB 1229 AACTTC 1234

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RESULT 4

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US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases

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FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,438  
; EARLIER FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 1814  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-347-801-9

Query Match 33.9%; Score 590; DB 3; Length 1814;  
Best Local Similarity 72.5%; Pred. No. 2.3e-158; Indels 0; Gaps 0;  
Matches 764; Conservative 0; Mismatches 290;

QY	189	GTCTCTATCGCCATGGCTGATGATAGGAGATGCTGCTGCTGTAGTGTGATGAGACATGAT	248
DB	321	GGCAGTATGAGCATAAAGGACGACAAAGGAGCTTGAAGATATTGTAGTCAATGGCAATGGG	380
QY	249	CAAGTCACTGGTCAATATTATCCACCAATCGGTGGCAAAATGCTGAACCAAAACAG	308
DB	381	GGCGAGCCTGGTCAATATGATGACCAATGATGGGAGAAATGGGAGCAAGCAG	440
QY	309	ACAAATAGTTTACATGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAA	368
DB	441	ACCAATAGTTTACATGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCCAA	500
QY	369	GCAAAATGTTTGGAGACTGGAGAAACCGTGGCGATATAAGAGGTTTTCGAAGATAGAAG	428
DB	501	GCAAGTGTCTTGAACCTGCTGAGACCGTAGCTATAAAAAAGGTTCTTCAAGACAAAGAG	560
QY	429	TACAAGAACCGAGAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTTGTTTG	488
DB	561	TACAAGAACCGAGCTGCAAAACCGAGTGTGTTGACCAACCAATGTGGTGGCTCTA	620
QY	489	AAGCATTTGCTCTTTTTCGACTACAGAGAAAGAGAGCTTTTCTTGAACCTTGGTTATGGAG	548
DB	621	AAGCATTTGCTCTTTTTCGACTACAGAGAAAGAGAGCTTTTCTTGAACCTTGGTTATGGAG	680
QY	549	TATGTCCTCGAGACGTTGTATCGAGTTCTGAACATTTATAGTAGTGCACAAACCAAGATG	608
DB	681	TATGTCCTCGAGACGTTGTATCGAGTTCTGAACATTTATAGTAGTGCACAAACCAAGATG	740
QY	609	CCTCTTGTCTATGTTAACTTTACAGTTATCAGATCTTCGGGGAGCTTGTCTACATTCAC	668
DB	741	CCTTTGATTTTCAAAACCTGTATATGATGATGATGATGATGATGATGATGATGATGATGAT	800

Qy	669	AGTTGCCGCGGAGTTTGTGACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGTATCCTCTT	728
Db	801	AACAGCAATTGGAGTGTGCCACAGGCAATTAAAGCCGCAAAATCTCTGGTTAAATCCTCAT	860
Qy	729	ACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTTGAACCA	788
Db	861	ACCATCAGCTTAAATTTGTGTGACTTTTGGCAGCGCGAAAGTTCTGGTTAAAGGGGAAACCA	920
Qy	789	AACATTTCTTACATCTGCTCACGATTTCTACCGTGCACCCGAGCTCATATTTGGTGCACCT	848
Db	921	AACATTTCTTACATCTGTTCTAGTACTACAGAGCTCCAGAGCTCATATTTGGTGTCTACT	980
Qy	849	GAGTACACAACCTCTATTGTATATCTGCTCTGCTGGTTGTGTTCTTGCTGAGCTTCTTCTT	908
Db	981	GAATACACAACAGCCATTGTATGTTTGGGTCTGCTGGCTGTGCTGCTGAGCTGCTTCTA	1040
Qy	909	GGTCAAGCCATTATTTCCCGGAGAAAATGCTGTGATCAGCTCGTGGGAAATATTATAAGTT	968
Db	1041	GGACAGCCTCTGTTTCCCTGGAGAAAGCGGTGTTGATCAGCTTGTTTGAAATCATCAAGTT	1100
Qy	969	CTTGGTACACCAACTCGAGAGAANAATCCGTTGTATGAATCCCACTACACAGATTTTCAAG	1028
Db	1101	CTGGGCACACCCACACGCTGAAGAAATTAAGTGATGAATCCAAATATATACCGAGTTTAA	1160
Qy	1029	TTCCACAGATAAAGGCCATCCCTGCGCACAGATCTTCCACAAAAGGATGCCCCAGAA	1088
Db	1161	TTCCCGCAAAATCAAAGCTCACCCATGGCATAAGAATATTCATATAAAGGATGCCCTGTGAA	1220
Qy	1089	GCGGTCAATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTTAAGATGCACAGCGCTC	1148
Db	1221	CGGTTAGATCTCGTGTCCAGGCTTCTCGAGTACTCACCAAAATCTTCGGTGCAGCTGCTTG	1280
Qy	1149	GAAGCTTTGTGCATCCGTTCTTTTGTATGAATCTACAGAGAACCAACGCTCGTGTTCACCAAT	1208
Db	1281	GAAGCATTTGTTCCATCCGTTCTTTTGTATGAATCTTCGGGATCCAAACACCCGCTTACCGAAT	1340
Qy	1209	GGAGCGCCTCTCCGCGCTCTCTTCAACTTCAAC	1242
Db	1341	GGTCGTTTTCTTCGCGCTCTCTTCAATTTTAAAG	1374

## RESULT 6

Qy	614	TGTC	TATG	TAAAC	TTT	CAC	AGT	TATC	AGAT	CTCT	CCG	GGC	AG	CTT	GC	T	TAC	AT	T	T	CAC	AG	TTG	673
Qy	614	TGTC	TATG	TAAAC	TTT	CAC	AGT	TATC	AGAT	CTCT	CCG	GGC	AG	CTT	GC	T	TAC	AT	T	T	CAC	AG	TTG	673
Db	629	GAT	TAT	TG	TAA	AACT	CT	TAT	AC	AGAT	CT	TTA	GG	CG	GT	TAT	CT	TAT	TAT	TAT	CT	CG	TTG	688
Qy	674	CCG	GG	AG	TTT	GT	C	AC	AG	AT	CT	TAA	AG	CT	CAAA	AT	CT	T	T	T	CG	TT	GAT	733
Db	689	TAT	TG	AG	T	CT	GC	AT	CC	AG	GT	AT	CA	AG	CT	CAAA	AT	CT	TAT	T	T	GG	T	748
Qy	734	TCA	AG	T	CAAA	AACT	CT	TG	TA	CT	TTT	GG	CA	GT	CG	AA	CA	AG	CT	CG	TTT	AAA	AG	793
Db	749	CC	AG	GT	TAA	AACT	TAT	TG	TA	CT	TTT	GG	AA	GT	CG	AA	AG	GT	TT	T	T	GG	CG	808
Qy	794	TT	CT	T	AC	AT	CT	CT	CA	AG	AT	CT	CA	CG	TG	CA	CC	CA	AG	CT	CA	TAT	TT	853
Db	809	AT	CA	T	AC	AT	AT	GT	CT	AG	AT	CT	TAT	AG	AG	CA	CT	AG	CT	CA	TAT	TT	GG	868
Qy	854	CAC	AA	CT	TT	CT	AT	TG	AT	TAT	CT	GG	T	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	913
Db	869	TAC	TAC	AG	CC	AT	TT	GA	CT	CT	GG	T	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	928
Qy	914	GCC	ATT	TAT	T	CC	CG	G	A	AA	AA	TG	CT	GT	GG	AT	CAG	CT	CG	T	GG	AA	AT	973
Db	929	GC	CT	CT	GT	TT	CC	CT	GG	TG	AG	AG	GG	AG	TT	GT	AG	AT	CAT	CA	AG	TT	CT	988
Qy	974	TAC	AC	CA	AA	CT	TCG	AGA	AG	AA	AA	CCG	TT	TG	AT	GA	AT	CC	CA	CT	AC	AT	CA	1033
Db	989	CAC	T	CC	CA	CA	CA	AG	GA	GAT	TAA	AG	TG	CA	TG	CA	TG	AA	CT	CA	AG	AT	TT	1048
Qy	1034	AC	AG	AT	AA	AG	GG	CC	CA	TCC	CT	GG	CA	CA	AG	AT	CT	TT	CC	CA	AA	AG	AT	1093

US-09-347-801-13  
; Sequence 13, Application US/09347801  
; Patent No. 6262345  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,438  
; EARLIER FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 13  
; LENGTH: 1429  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1202)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1237)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1297)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1340)  
; FEATURE:

Db 1049 ACAGATTAAAGCACATCCATGTCACAAAGATCTTCCATAAGCGCATGCCCTCCAGAGGCTGT 1108  
QY 1094 TGATTTGGCATCAAGGCTCTTCAATACCTCCAGTCTAAGATGACAGAGCGCTCGAAGC 1153  
Db 1109 TGATTTGGTATCAAGACTACTACAACTACTCCCTTAACTTGGCGTGACAGATTTTAGATGC 1168  
QY 1154 TTGTGCACATCCGTT---CTTTGATGAATCAGAGAACCAAAACGCTCGCTTTTACCAAAATGG 1210  
Db 1169 CTTGGACGACCTTTCTTTGGACGAATTCGNGATCCAAATCTCGCTTGGCAANTGG 1228  
QY 1211 ACGGCTCTCCCGGCTCTCTTCAACTTCAAAACAA 1244  
Db 1229 GCGATCCNTCCAACTAATTAATTCAAACCCA 1262

## RESULT 7

US-09-854-731-13  
; Sequence 13, Application US/09854731  
; Patent No. 6794561  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 13  
; LENGTH: 1429  
; TYPE: DNA  
; ORGANISM: Glycine max

## FEATURE:

NAME/KEY: unsure  
LOCATION: (1202)  
NAME/KEY: unsure  
LOCATION: (1237)  
NAME/KEY: unsure  
LOCATION: (1297)  
NAME/KEY: unsure  
LOCATION: (1340)  
NAME/KEY: unsure  
LOCATION: (1376)  
NAME/KEY: unsure  
LOCATION: (1410)  
NAME/KEY: unsure  
LOCATION: (1416)

US-09-854-731-13

Query Match 30.5%; Score 530.4; DB 4; Length 1429;

Best Local Similarity 69.5%; Pred. No. 2.3e-141;

Matches 733; Conservative 0; Mismatches 318; Indels 3; Gaps 1;

QY 194 TATCGCATGGCTGATGATGAAGAGAGATCGCTGCTGTAGTTGATGGACATCATCAAGT 253  
Db 209 TATGAANATTAGGANTGATAGAAATGAGCCACAGTTGTTGATGGCAACGGAACGGA 268  
QY 254 CACTGGTGCATATTATTTCCACCAATTCGGTGGCAAAATGGTGAACCAAAACAGACAAT 313  
Db 269 GACAGGACATATCATTTGTGACTACCATTGGGGGTAGAAATGGTCAAGCAAGCAGACTAT 328  
QY 314 TAGTTACATGGCGGAGGAGTGTGTTGGTACAGGCTGTTCCGGATCGTTTCCAAACAA 373  
Db 329 AAGCTACATGGCAGAGCGTGTGTAGGGCATGATCATTTGGAGTTGTCTTCCAGGCTAA 388  
QY 374 ATGTTGGAGACTGGGAACCGTGGCGATAAAGAGGTTTTTCAAGATAGAATACAA 433  
Db 389 GTGCTTGGAAACCGTGAACCTGTGGCTATCAAAAGGTTCTTCAAGACAGAGGTACAA 448  
QY 434 GAACCGAGAACTTCAGTTGATCGGTGTGATGGAATCATCCGAATGTGGTTTGTGAAGCA 493

Db 449 GAACCGGAGCTGCAAAACAAATCGCGCTTCTTGACCACCAACCAATGTGTTGCTTTGAAGCA 508  
QY 494 TTGCTCTTTTTCGACTACAGAGAAAGAGAGAGCTTTTCTTGAACCTTGGTTATCGAGTATGT 553  
Db 509 CTGTTCTTTTTCGACTACAGAGAAAGAGAGCTTTTCTTGAACCTTGGTTATCGAGTATGT 568  
QY 554 CCCTGAGAGCTTGTATCCAGTTCTGAAACATTTATAGTAGTGCAAAACCAAGAAATGCTCTCT 613  
Db 569 TCCTGAACAGTTAATCGGCTGATTAACCAATTTACCAAGTTTAAACCAAGGATGCCACT 628  
QY 614 TGTCTATGTTAACTTTTACAGTTTACAGATCTTCCGGGAGCTTGTCTTACATTCACAGTTG 673  
Db 629 GATATATGAAACTCTATACATACAGATCTTTAGGGCGTTTATCTTATATTCATCGCTTG 688  
QY 674 CCGGGAGTTTGTACAGAGATCTAAAGCTCAAAATCTTCTGGTTGATGCTCTTACTCA 733  
Db 689 TATTGGAGTCTGCCATCGGGATATCAAGCTCAAAATCTTATGGTCAATCCACACACTCA 748  
QY 734 TCAAGTCAAAATCTGTGACTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAACCAACAT 793  
Db 749 CCAGGTTAAATTTATGTGACTTTGGAAGTGCAGAGTTTGGTAAAGGCGAACCAATAT 808  
QY 794 TTCTTACATCTGCTCACAGATCTACCGTGCACCGAGCTCATATTTGGTGCACACTGAGTA 853  
Db 809 ATCATACATATGTTCTAGATACCTATAGAGCACTCTGAGCTCATATTTGGGCGCAACTGA 868  
QY 854 CACAACTTCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGCTGAGCTTCTTCTGCTGCA 913  
Db 869 TACTACAGCAATGAGCTCTGCTGCTGTTGGATGTTTGTAGCTGAGCTGCTGCTTGGACA 928  
QY 914 GGCATTTATTTCCCGGAGAAATGCTGTGATCAGCTCGTGGAAATTTATTAAGTTCTTGG 973  
Db 929 GCCTCTGTTCCCTGGTGGAGTGGAGTTGATCAACTTTGTTGAGATCATCAAGGTTCTGG 988  
QY 974 TACACCACTCGAGAGAAATCCGTTGTATGATGATGATGATGATGATGATGATGATGATG 1033  
Db 989 CACTCCAAAGGAGAGATTAAGTGCATGAACCCCTAAATTTATACAGAAATTTAAATTC 1048  
QY 1034 ACAGATAAGGCGCCATCCCTGGCAGAGATCTTCCAAAGAGATGCGCCCGCAGAGCGT 1093  
Db 1049 ACAGATTAAAGCACATCCATGGCAGCAAGATCTTCCATAAGCATGCTCCAGAGGCTGT 1108  
QY 1094 TGATTTGGCATCAAGGCTGCTTCAATCTCTCCAGTCTTAAGATGACAGCGCTCGAAGC 1153  
Db 1109 TGATTTGGTATCAAGACTACTACATCTCCCTTAACCTTGGGTGCACAGTTTGTAGATGC 1168  
QY 1154 TTGTGCACATCCGTT---CTTTGATGAATCAGAGAACCAACGCTCGTTTACCAAAATGG 1210  
Db 1169 CTTGGACGACCTTTCTTTGGACGAATTCGNGATCCAAATCTCGCTTGGCAANTGG 1228  
QY 1211 ACGGCTCTCCCGGCTCTCTTCAACTTCAAAACAA 1244  
Db 1229 GCGATCCNTCCAACTAATTAATTCAAACCCA 1262

## RESULT 8

US-09-566-921-24  
; Sequence 24, Application US/09566921  
; Patent No. 6682888  
; GENERAL INFORMATION:  
; APPLICANT: Loring, Jeanne F.  
; APPLICANT: Tingley, Debora W.  
; APPLICANT: Edwards, Carla M.  
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE  
; FILE REFERENCE: PA-0024 US  
; CURRENT APPLICATION NUMBER: US/09/566,921  
; CURRENT FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PERL Program  
; SEQ ID NO 24  
; LENGTH: 1952  
; TYPE: DNA  
; ORGANISM: Homo sapiens



Db 1070 GACCAGTGTGGAGATCATAGGTGCTGGGAACCAACCGGGAACAAATCCGAGAG 1129  
QY 1002 ATGAATCCCACTACACAGATTTCAAGTTCCCAACAGATAAAGCCCATCCCTGGCACAAG 1061  
Db 1130 ATGAACCCCACTACACAGGATTTCAAGTTCCCTCAGATTAAAGCTCACCCCTGGACAAAG 1189  
QY 1062 ATCTTCCACAAAAGGATGCCCCAGAAAGCGTTGATTGTCATCAAGGCTGCTTCAATAC 1121  
Db 1190 GTGTTCAATCTGAACGCCCGCAGAGGCCATCGCGCTGTGCTTAGCTGTGGAGTAC 1249  
QY 1122 TCTCCAGTCTAAGATGCAAGCGCTCGAAGCTTTGTCACATCCGTTCTTTGATGAATC 1181  
Db 1250 ACCCATCTCAAGGCTCTCCCACTAGAGCGCTGTGGCAGACAGCTTCTTTGATGAATG 1309  
QY 1182 AGAGAACCAACCGCTGTTTACCAATAGGAGCGCTCTCCGCGCTCTCTTCAACTTCA 1239  
Db 1310 CGATGTCTGGGAACCCAGCTGCTTAACAACCGGCCACTTCCCGCTCTCTTCAACTTCA 1367

## RESULT 10

US-08-602-264A-1  
; Sequence 1, Application US/08602264A  
; Patent No. 5837853  
; GENERAL INFORMATION:  
; APPLICANT: Akihiko TAKASHIMA et al.  
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR  
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE  
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WENDEROFF, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 144 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,264A  
; FILING DATE: February 20, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/204,091  
; FILING DATE: March 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE:  
; TELEFAX:  
; TELEX:

## INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2088 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna to genomic RNA  
; ORIGINAL SOURCE:  
; ORGANISM: human being  
US-08-602-264A-1

Query Match 22.6%; Score 393.2; DB 2; Length 2088;

Best Local Similarity 63.3%; Pred. No. 5.7e-102;  
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;

QY 305 ACACACAATTAGTTACATGCGGAGCGAGTTGTTGTTACAGGCTCGTTTCGGGATCGTTTT 364

Db 768 ACAAGAGTCAGCTATACAGACACTAAACTCATTTGGAAATGGATCATTTTGGTGTGTATA 827  
QY 365 CAAGCAAAATGTTGGAGACTGGAGAAACCGTGGCGATAAAGAGAGTTTTCGAAGATAG 424  
Db 828 TCAAGCCAAACTTTGTGATTCAGGAGAACTGGTGCACATCAAGAAAGTATTCGAGACAA 887  
QY 425 AAGATACAAGAACCCGAGAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGCTTGG 484  
Db 888 GAGATTTAAGATTCAGAGCTCCAGATCATGAGAAGCTAGATCATCTGTAAACATAGTCCG 947  
QY 485 TTTGAAGCATTCCTTCTTTTCGACTACAG---AGAAAGACGAGCTTTTCTTGAACCTTGT 541  
Db 948 ATTGCGTATTATTTCTTCTACTCCAGTGGTCAGAAGAAAGATGAGGTCTATCTTAACTCG 1007  
QY 542 TATGAGATGATGCCCTCGAGACGTTGATCGAGTTCTGAAACATATATAGTAGTGCACAA 601  
Db 1008 GCTGGACTATGTTCCGGAACAGATATACAGAGTTGCCAGACATATAGTCGAGCCAAACA 1067  
QY 602 AAGATGCGCTCTGTCTATGTTAAACTTTACAGTTATCAGATCTTCCGGGAGCTTCTCTTA 661  
Db 1068 GACGCTCCCTGTGATTTATGTCAGTTGATATGATCAGCTGTTCCGAAGTTTACCTTA 1127  
QY 662 CATTCACAGTTGCGCGGAGTTTGTACAGAGATCTAAAGCCCTCAAAATCTTCTGTGTTGA 721  
Db 1128 TATCCA---TTCCTTTTGAATCTGCCATCGGATATTAACCGCAGACCTCTTGTGTTGA 1184  
QY 722 TCTCTTACTCATCAAGTCAAAATCTGTGACTTTGTCAGTTGCGAGTGCAGAACAGCTCGTTAA 781  
Db 1185 TCTGATACTGCTGTATTAATAAATCTGTGACTTTTGGAAAGTGCAGAGCAGCTGTGTCGAG 1244  
QY 782 TGAACCAAACTTCTTACATCTGCTCAGATTCTACCGTGCACCCGAGCTCATATTTGG 841  
Db 1245 AGAACCAATGTTTGTATATCTGTTCTCGTACTATAGGGACACAGAGTTGATCTTTGG 1304  
QY 842 TGCCTACTGAGTACACAACTTCTATTGATATCTGCTGCTGCTGTTGTTCTTGTCTGAGCT 901  
Db 1305 AGCCACTGATTATACCTCTAGTATAGATGATGTTGCTGCTGCTGTTGTTGCTGAGCT 1364  
QY 902 TCTTCTTGTGTCAGCATTAATTCCTCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATTA 961  
Db 1365 GTTACTAGGACAAACCAATATTTCCAGGGGATAGTGGTGTGGATCAGTTGGTAGAATAAT 1424  
QY 962 TAAAGTTCTTGGTACACCAACTCGAGAAGAAATCCGTTGATGAATCCCAACTACACAGA 1021  
Db 1425 CAAGGTCCTGGGAATCTCAACAGGAGGCAATCAGAGAAATGAAACCAACTACACAGA 1484  
QY 1022 TTTCAAGTTCCCAAGATAAAGCCCATCCCTGGCAAGATCTTCCACAAAAGGATGCC 1081  
Db 1485 ATTTAAATTCCTCAAAATTAAGGCACATCCTTGGACTAAGGTCTTCCGACCCCGAACTCC 1544  
QY 1082 CCGAAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCAC 1141  
Db 1545 ACCGAGGCAATTTGCACTGTAGCCGTCTGTGGAGTATACACCAACTGCCCGACTAAC 1604  
QY 1142 AGCGCTCGAAGCTTGTGCACATCCGTTCTTTGATGAACCTCAGAGAACCACCAACCGCT 1201  
Db 1605 ACCACTGGAGCTTGTGCACTTCAATTTTGTGATTAATACGGGACCAATGTCAACT 1664  
QY 1202 ACCAAATGGACGGCCTCTCCCGCTCTCTTCAACTTCAACAAAGAGTAGCTGGATCATC 1261  
Db 1665 ACCAAATGGCGAGACACACCTGCACTCTTCAACTTCCACCTCAAGAACTGTCAAGTAA 1724  
QY 1262 ACCTGAACCTGGTCAACAAGTTGATTCAGACGATATCAAGAGACAA 1307  
Db 1725 TCCACCTCTGGCTACCATCCTTATTCCTCTCATGCTCGGATTCNA 1770

## RESULT 11

US-08-461-018A-1  
; Sequence 1, Application US/08461018A  
; Patent No. 6071694  
; GENERAL INFORMATION:

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; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROOTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-08-461-018A-1

Query Match 22.6%; Score 393.2; DB 3; Length 2088;
Best Local Similarity 63.3%; Pred. No. 5,7e-102;
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;

QY 305 ACAGACAATTACTATGTCGGGCGGAGCTTCTGTGACAGGCTGTTCCGAGCTGTTT 364
DB 768 ACAGAGTCAGCTATACAGACACTAACTCATTTGGAATGGATCATTTGGTGGTATA 827
QY 365 CCAAGCAAAATGTTGGAGACTGGAGAACCCGTGGCGATTAAGAAAGGTTTTCAGAGATAG 424
DB 828 TCAAGCCAACTTTGTGATTACAGAGAACTGTCGCCATCAAGAAAGTATTGCAGACAA 887
QY 425 AAGATACAGAACCCGAGAACTTCAGTTGATGCGGTGATGATCATCCGAATGTCGTTG 484
DB 888 GAGATTAAAGATCCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTC 947
QY 485 TTTGAGCAATCTCTCTTTTCCAGTACAG- --AGAAAGACGAGCTTTTCTGAACTTGGT 541
DB 948 ATTGGCGTTATTTCTTCTACTCCAGTGGTGAAGAAAGATGAGGTCATCTTAAATCTGTT 1007
QY 542 TATGAGTATGTCCTCTGAGACGCTGTATCGAGTCTTGAAACATATTAGTAGTGCAAAACA 601
DB 1008 GCTGAGCTATGTTCCGAAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACA 1067
QY 602 AAGATGCTCTGTGTATGTTAACTTTACAGTTATACAGATCTTCCGGGAGCTTTCGTTA 661
DB 1068 GACGCTCCCTGTGATTATGTCAAGTTGTATATGATGATCAGCTGTTCCGAAAGTTAGCCTA 1127
QY 662 CATTACAGTTCCTCCGGGAGTTTGTACAGAGATCTTAAGCCTCAAAATCTTCTGTTGA 721
DB 1128 TATCCA---TTCCTTTGGAATCTGCCATCGGAGATATTAAACCCGAGAACTCTTGTGGA 1184

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RESULT 12
US-09-216-958-1
; Sequence 1, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROOTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,958
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,018
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367

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QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACATTTGGCGAGTGGAAACAGCTCGTTAAAGG 781
DB 1185 TCCTGATACTGCTGTATTAATAACTCTGTGACTTTTGGAAAGTGCAGAGCAGCTGTCGAGG 1244
QY 782 TGAACCAACAATTTCTTACATCTGTCTACAGTTCTACCGTGCACCGGAGCTCATATTTGG 841
DB 1245 AGAACCCAAATGTTTCGTATATCTGTTCGGTACTATAGGCGACCAAGAGTTGATCTTTGG 1304
QY 842 TGCCACTGAGTACACAACTTCTATTGATATCTGTGCTGTCTGCTGTGTTGTTCTTCTGAGCT 901
DB 1305 AGCCACTGATTATACCTCTAGTATAGATGATGTTGCTGTGCTGTGTTGCTGAGCT 1364
QY 902 TCTTCTGCTGAGCCATTTATTTCCCGGAGAAATCTGTGTGATCAGCTCGTGGAAATTTAT 961
DB 1365 GTTACTAGGACAAACCAATATTTCAGGGGATAGTGTGTGGATCAGTTTGGTGAATAAT 1424
QY 962 TAAAGTTCTTGTGATACCAACTCCGAGAGAAATCCGTTGTATGAAATCCCAACTACACAGA 1021
DB 1425 CAAGTCTCTGGAACTCCAAACAGGGAGCAATAGAGAAATGAACCCAACTACACAGA 1484
QY 1022 TTTCAAGTTCCACAGATAAAGGCCCATCCCTGGGCACAAAGATCTTCCACAAAGAGTGC 1081
DB 1485 ATTAAATTCCTCAATTAAGGCACATCCTTGGACTAAGGCTTCCGACCCGAGACTCC 1544
QY 1082 CCCAGAACGGTTGATTGGGATCAAGGCTGCTTCAATATCTTCAAGTCTTAAGATGCAAC 1141
DB 1545 ACCGGAGGCAATTGCACTGTGTAGCCGCTGTCTGGAGTATACACCAACTGCCCGACTAAC 1604
QY 1142 AGCGTCTGAAGCTTGTGCACATCCGTTCTTTGATGAACTCAGAGAACCAAAAGCTCGTTT 1201
DB 1605 ACCACTGGAAGCTTGTGCACATTTCAATTTTGTGAAATTAACGGACCCCAAAATGTCAA 1664
QY 1202 ACCAAATGGAGGCGCTCTCCGCGCTCTCTTCAACTTTCAAAACAAAGTAGCTGGATCATC 1261
DB 1665 ACCAAATGGCGAGACACACCTGCACTCTTCAACTTCCACTCAGAACTGTCAAGTAA 1724
QY 1262 ACTTGAACTGTCACAAAGTTGATTCCAGACAAATATCAAGAGACAA 1307
DB 1725 TCCACCTCTGCTACCATCTTATTTCTCTCTCATCTCGGATTCAA 1770

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; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-09-216-958-1

Query Match      22.6%; Score 393.2; DB 3; Length 2088;
Best Local Similarity 63.3%; Pred. No. 5.7e-102;
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;

QY 305 ACAGACAATTAGTTACATGCGGAGCGAGTTGTTGTACAGGCTCGTTCCGGATCGTTTT 364
DB 768 ACAAGAGTCAGCTATACAGACATAAATCTCATTTGAAATGGATCATTTGGTGTGTATA 827
QY 365 CCAAGCAAAATGTTTGGAGACTCGAGAACCCGTCGCATATAAGAGGTTTTCAGATAG 424
DB 828 TCAGGCCAACTTTGTGATTCAGAGAACTGTCGCATCAAGAAAGTATTGCAGACAA 887
QY 425 AGATACAAAGAACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGTGTTTG 484
DB 888 GAGATTTAAGAAATCGAGAGCTCCAGATCATAGAAAGCTAGATCACTGTAAACATAGTCG 947
QY 485 TTGTAGGACTGCTTTCTTTTCGACTACAG---AGAAAGCAGCTTTTCTTGAACCTTGT 541
DB 948 ATTGCGTTATTCTTTCTACTCCAGTGTGAGAAAGAAAGATGAGGTCTATCTTAATCTGT 1007
QY 542 TATGGAGTAGTCCCTCGAGACGTTGTATCGAGTTCTGAAACATATATAGTAGTCAAAACA 601
DB 1008 GCTGGACTATGTTCCGAAACAGTATACAGAGTTGCGACACATATAGTCGAGCCAAACA 1067
QY 602 AAGAAATGCTTGTCTATGTTTAACTTTACAGTTATCAGATCTTCGGGGAGCTTCCTTA 661
DB 1068 GACGCTCCCTGTGATTATGTCAGGTTGATATGATATGATCAGCTGTTCCGAAGTTTAGCCTA 1127
QY 662 CATTACAGTTGCGCGGAGTTGTCACAGAGATCTTAAGACCTCAAAATCTTCTGTTGA 721
DB 1128 TATCCA---TTCTTTTGGAACTGCGCATCGGATATTTAAACCGCAGAACCTCTGTGTGA 1184
QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTGCAGAACAGCTCGTTAAAGG 781
DB 1185 TCCTGATACCTGTATTAAACTCTGTGACTTTTGGAAAGTGCAGACGCTGTCGAGG 1244
QY 782 TGAACCAAAATTTTACATCTGCTCAAGATTCACCGTGACCCGAGCTCATATTGG 841
DB 1245 AGAACCCAATGTTTCGTATATCTGTTCTCGGTACTATAGGACACAGAGTTGATCTTTGG 1304
QY 842 TGCCTAGTGTACACAACTCTATGATATCTGCTGCTGCTGTTGTTCTGCTGAGCT 901
DB 1305 AGCCACTGATATACCTCTAGTATAGATGATGTTGCTGCTGCTGTTGTTGCTGAGCT 1364
QY 902 TCTTCTTGGTCAGCAATTTATCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATAT 961
DB 1365 GTTACTAGGACACCAATATTTCCAGGGGATAGTGGTGTGGATCAGTTGTTAGAAATAT 1424
QY 962 TAAAGTTCTTGGTACACCAATCTCGAGAGAAATTCGGTTGATGAAATCCCAACTACACAGA 1021
DB 1425 CAAGGTCCTGGAACTCCAAACAGGGAGCAAAATCAGAGAAATGAAACCCAACTACACAGA 1484
QY 1022 TTTCAGTTCCACAGATAAGGCCATCCCTGGCACAGATCTTCCACAAAAGGATGCC 1081
DB 1485 ATTAAATCCCTCAAAATTAAGGCACATCTTGGACTTAAGGTTCTTCGACCCCGAATCC 1544
QY 1082 CCCAGAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCAC 1141

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RESULT 13
US-09-489-765A-3
; Sequence 3, Application US/09489765A
; Patent No. 6323029
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
; FILE REFERENCE: RTS-0124
; CURRENT APPLICATION NUMBER: US/09/489, 765A
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-09-489-765A-3

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Query Match      22.5%; Score 391.6; DB 3; Length 1389;
Best Local Similarity 63.2%; Pred. No. 1.3e-101;
Matches 636; Conservative 0; Mismatches 364; Indels 6; Gaps 2;

QY 305 ACAGACAATTAGTTACATGCGGAGCGAGTTGTTGTACAGGCTCGTTCCGGATCGTTTT 364
DB 192 ACAGAGTCAGCTATACAGACACTAAAGTATTGAAATGATCATTTGGTGTGTATA 251
QY 365 CCAAGCAAAATGTTTGGAGACTGGAGAACCCGTCGCATATAAGAGGTTTTCAGAGTAG 424
DB 252 TCAAGCCAAACTTTGTGATTCAGAGAACTGTCGTCATCAAGAAAGTATTGCAGGACAA 311
QY 425 AGATACAAAGAACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGTGTTTG 484
DB 312 GAGATTTAAGAAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCATCTGTAACATAGTCG 371
QY 485 TTGTGAAGCATGCTTCTTTTCGACTACAG---AGAAAGCAGCTTTTCTTGAACCTTGT 541
DB 372 ATTGCGTTATTCTTCTACTCCAGTGTGAGAGAAAGATGAGTCTATCTTAATCTGTT 431
QY 542 TATGGAGTAGTCCCTCGAGACGTTGATCGAGTTCTTGAAACATATATAGTAGTCAAAACA 601
DB 432 GCTGGACTATGTTCCGAAACAGTATACAGAGTTGCGACACATATAGTCGAGCCAAACA 491
QY 602 AAGATGCTCTTGTCTATGTTTAACTTTACAGTTATCAGATCTTCGGGGAGCTTCCTTA 661
DB 492 GACGCTCCCTGTGATTTGTCAAGTTGATATGATGATGATGATGATGATGATGATGATGAT 551
QY 662 CATTACAGTTGCGCGGAGTTTGTCAAGAGATCTTAAAGCCTCAAAATCTTCTGTTGA 721
DB 552 TATCCA---TTCTTTTGGAACTGCGCATCGGATATTAACCGCAGAACTCTTGTGGA 608
QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTTCGGAACAGCTCGTTAAAGG 781

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Result No.	Score	Query Match	Length	DB	ID	Description
1	1431.6	82.4	1490	21	US-10-477-687-12	Sequence 14, Appl
2	1099.8	63.3	1143	9	US-09-938-842A-875	Sequence 875, App
3	1099.8	63.3	1143	11	US-09-938-842A-875	Sequence 875, App
4	1058.4	60.9	1621	16	US-10-392-408-15	Sequence 15, Appl
5	768.6	44.2	1726	18	US-10-425-114-12807	Sequence 12807, A
6	759.2	43.7	1979	18	US-10-424-599-67990	Sequence 67990, A
7	750.2	43.2	1881	18	US-10-424-599-67987	Sequence 67987, A

Best local similarity 50.00; local no.: 0;  
Matches 1460; Conservative 0; Mismatches 29; Indels 1; Gaps 1;



Db 181 GAGACTGGAGAACCGTGGCGATAGAAGAGTTTTCAGAGATAGAAGATACAAGAACCGA 240  
 Qy 441 GAACCTTCAGTGTGATGCGTGTGATGATCATCCGAATGCTGTTTGTGTTGAAGCATTCCTTC 500  
 Db 241 GAACCTTCAGTGTGATGCGTGTGATGATCATCCGAATGCTGTTTGTGTTGAAGCATTCCTTC 300  
 Qy 501 TTTTCGACTACAGAGAAAGACGAGCTTTCTTGAACCTTGTGTTATGAGTATGCTCCTGAG 560  
 Db 301 TTTTCGACTACAGAGAAAGACGAGCTTTCTTGAACCTTGTGTTATGAGTATGCTCCTGAG 360  
 Qy 561 AGCTTGTATCGAGTCTTGAACATATATAGTAGTGAACCAAGAAAGTGCCTTCTGCTAT 620  
 Db 361 AGCTTGTATCGAGTCTTGAACATATATAGTAGTGAACCAAGAAAGTGCCTTCTGCTAT 420  
 Qy 621 GTTAACTTTACAGTATCAGATCTTCCGGGACCTTGTATCAATTCAGAGTTGCCCGGGA 680  
 Db 421 GTTAACTTTACAGTATCAGATCTTCCGGGACCTTGTATCAATTCAGAGTTGCCCGGGA 480  
 Qy 681 GTTTCGTCAGAGATCTAAAGCCTCAAAATCTTCTGTTGATCCTTACTCATCAAGTC 740  
 Db 481 GTTTCGTCAGAGATCTAAAGCCTCAAAATCTTCTGTTGATCCTTACTCATCAAGTC 540  
 Qy 741 AAAATCTGTGACTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC 800  
 Db 541 AAAATCTGTGACTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC 600  
 Qy 801 ATCTGCTACAGTATCTACCGTCCACCGAGCTCATATTTGGTGCACCTGAGTACAACT 860  
 Db 601 ATCTGCTACAGTATCTACCGTCCACCGAGCTCATATTTGGTGCACCTGAGTACAACT 660  
 Qy 861 TCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGAGCTTCTTCTGGTCAGGCATTA 920  
 Db 661 TCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGAGCTTCTTCTGGTCAGGCATTA 720  
 Qy 921 TTCCCGGAGAAATGCTGTGATCAGCTCGTGGGAAATTTAAAGTTCTTGGTACACCA 980  
 Db 721 TTCCCGGAGAAATGCTGTGATCAGCTCGTGGGAAATTTAAAGTTCTTGGTACACCA 780  
 Qy 981 ACTCGAGAGAAATCGTTGTATGATCCAACTACACAGATTTCAAGTTCCACAGATA 1040  
 Db 781 ACTCGAGAGAAATCGTTGTATGATCCAACTACACAGATTTCAAGTTCCACAGATA 840  
 Qy 1041 AAGGCCATCCCTGGCAGAGATCTTCCAAAGAGTGCCTCCCGAGAGCGGTTGATTG 1100  
 Db 841 AAGGCCATCCCTGGCAGAGATCTTCCAAAGAGTGCCTCCCGAGAGCGGTTGATTG 900  
 Qy 1101 GCATCAAGGCTCTTCAATPACTCTCAAGTCTAAGATGCACAGCGCTGAAAGCTTGTGCA 1160  
 Db 901 GCATCAAGGCTCTTCAATPACTCTCAAGTCTAAGATGCACAGCGCTGAAAGCTTGTGCA 960  
 Qy 1161 CATCGGTTCTTTGATGAACTCAGAGAACCAACGCTCGTTTACCAAAATGGACGGCTCTC 1220  
 Db 961 CATCGGTTCTTTGATGAACTCAGAGAACCAACGCTCGTTTACCAAAATGGACGGCTCTC 1020  
 Qy 1221 CGGCTCTCTTCAACTTCAACAGAGTAGTGTGATCATCCTGAACTGCTGAACAG 1280  
 Db 1021 CGGCTCTCTTCAACTTCAACAGAGTAGTGTGATCATCCTGAACTGCTGAACAG 1080  
 Qy 1281 TTGATTCAGACCATATCAAGAGACAAATTTGGGCTTAAGCTTCTGAATCAATCTGAACT 1340  
 Db 1081 TTGATTCAGACCATATCAAGAGACAAATTTGGGCTTAAGCTTCTGAATCAATCTGAACT 1140  
 Qy 1341 TAA 1343  
 Db 1141 TAA 1143

RESULT 3

US-09-938-842A-875  
 ; Sequence 875, Application US/09938842A  
 ; Publication No. US20040009476A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel  
 ; APPLICANT: Wang, Xun  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE  
 ; FILE REFERENCE: SCRIPI300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 875  
 ; LENGTH: 1143  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-938-842A-875

Query Match 63.3%; Score 1099.8; DB 11; Length 1143;  
 Best Local Similarity 97.6%; Pred. No. 7.5e-307;

Matches 1116; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 201 ATGGCTGATGATAGGAGATGCTCTGCTGTGTGATGACATGATCAAGTCACTGCT 260  
 Db 1 ATGGCTGATGATAGGAGATGCTCTGCTGTGTGATGACATGATCAAGTCACTGCT 60  
 Qy 261 CATATTATTTCCACCACCAATCGGTGGCAAAATGTTGAAACCAACCAACCAATTTAGTTAC 320  
 Db 61 CATATTATTTCCACCACCAATCGGTGGCAAAATGTTGAAACCAACCAACCAATTTAGTTAC 120  
 Qy 321 ATGGCGGACGAGTTGTTGGTACAGGCTCGTTCCGGGATCGTTTCCAGCAAAATGTTTG 380  
 Db 121 ATGGCGGACGAGTTGTTGGTACAGGCTCGTTCCGGGATCGTTTCCAGCAAAATGTTTG 180  
 Qy 381 GAGACTGAGAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAAGATACAAGAACCGA 440  
 Db 181 GAGACTGAGAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAAGATACAAGAACCGA 240  
 Qy 441 GAACTTCAGTTGATGCGTGTGATGATCATCCGAATGCTGTTTGAAGCATTCGCTTC 500  
 Db 241 GAACTTCAGTTGATGCGTGTGATGATCATCCGAATGCTGTTTGAAGCATTCGCTTC 300  
 Qy 501 TTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTATGAGTATGCTCCTGAG 560  
 Db 301 TTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTATGAGTATGCTCCTGAG 360  
 Qy 561 AGCTTGTATCGAGTCTGAAACATTTATAGTAGTGAACCAAGAAATGCTCTTGTCTAT 620  
 Db 361 AGCTTGTATCGAGTCTGAAACATTTATAGTAGTGAACCAAGAAATGCTCTTGTCTAT 420  
 Qy 621 GTTAACTTTACAGTATCAGATCTTCCGGGACCTTGTATCAATTCAGAGTTGCCCGGA 680  
 Db 421 GTTAACTTTACAGTATCAGATCTTCCGGGACCTTGTATCAATTCAGAGTTGCCCGGA 480  
 Qy 681 GTTTCGTCAGAGATCTAAAGCCTCAAAATCTTCTGTTGATCCTTACTCATCAAGTC 740  
 Db 481 GTTTCGTCAGAGATCTAAAGCCTCAAAATCTTCTGTTGATCCTTACTCATCAAGTC 540  
 Qy 741 AAAATCTGTGACTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC 800  
 Db 541 AAAATCTGTGACTTTGGCAGTCGGAACAGCTCGTTTAAAGGTGAACCAAAATTTCTTAC 600  
 Qy 801 ATCTGCTACAGATCTACCGTCCACCGAGCTCATATTTGGTGCACCTGAGTACAACT 860  
 Db 601 ATCTGCTACAGATCTACCGTCCACCGAGCTCATATTTGGTGCACCTGAGTACAACT 660  
 Qy 861 TCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGAGCTTCTTCTGGTCAGGCATTA 920  
 Db 661 TCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGAGCTTCTTCTGGTCAGGCATTA 720

QY 921 TTCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTAATAAGTCTTGGTACACCA 980  
 DB 721 TTTCCTGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTAATAAGTCTTGGTACACCA 780  
 QY 981 ACTCGAAGAAATCCGTTGTATGAATCCCAACTACACAGATTCAAGTTCCACAGATA 1040  
 DB 781 ACTCGAAGAAATCCGTTGTATGAATCCCAACTACACAGATTCAAGTTCCACAGATA 840  
 QY 1041 AAGGCCATCCCTGGGACAGATCTTCCACAAAGGATGCCCCAGAGCGTTGATTGG 1100  
 DB 841 AAGGCACATCCCTGGGACAGATCTTCCAAAGGATGCCCCAGAGCGATTGATTGTT 900  
 QY 1101 GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA 1160  
 DB 901 GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCA 960  
 QY 1161 CATCCGTTCTTGGATGAATCAAGAACCAACGCTCGTTTACCAATGGAGCGGCTCTC 1220  
 DB 961 CATCCGTTCTTGGATGAATCAAGAACCAACGCTCGTTTACCAATGGAGCGGCTCTC 1020  
 QY 1221 CGGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAG 1280  
 DB 1021 CGGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAG 1080  
 QY 1281 TTGATTTCCAGACCATATCAAGACAAATGGGTCTAAGCTTCTTGAATCAATCTGGAAT 1340  
 DB 1081 TTGATTTCCAGACCATATCAAGACAAATGGGTCTAAGCTTCTTGAATCAATCTGGAAT 1140  
 QY 1341 TAA 1343  
 DB 1141 TAA 1143

RESULT 4

US-10-292-408-15  
 ; Sequence 15, Application US/10292408  
 ; Publication No. US20030182692A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN THIELEN, NOCHA  
 ; APPLICANT: DA COSTA E SILVA, OSWALDO  
 ; APPLICANT: CHEN, RUOYING  
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS  
 ; TITLE OF INVENTION: OF USE IN PLANTS  
 ; FILE REFERENCE: 16313-0178  
 ; CURRENT APPLICATION NUMBER: US/10/292,408  
 ; PRIOR FILING DATE: 2002-11-12  
 ; PRIOR FILING DATE: 60/346,096  
 ; NUMBER OF SEQ ID NOS: 51  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 15  
 ; LENGTH: 1621  
 ; TYPE: DNA  
 ; ORGANISM: Brassica napus  
 US-10-292-408-15

Query Match 60.9%; Score 1058.4; DB 16; Length 1621;  
 Best Local Similarity 81.5%; Pred. No. 8.9e-295;  
 Matches 1307; Conservative 0; Mismatches 271; Indels 26; Gaps 6;  
 QY 75 TCCTCTCTCTCTCTATCGGCACATGATCATGACCAACCAAACTGATTGAAACTCATTT 134  
 DB 8 TCCTCTCTCTCTCTCCACATTTGATGATCATTTACCAACCAAACTAATTGAAATCCATTT 67  
 QY 135 GTCTCTCTCTCTCAAAATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 194  
 DB 68 GTTCT 125  
 QY 195 ATCGCCATGGCTGATGATAGGAGAT---GCCCTGCTGCTGCTAGTGTGATGGACATGATCAA 251  
 DB 126 AAGCTCATGGCTGACGATAGGGAGATGCCCGGCTGCTGTAGTGTGATGGACATGACCAA 185  
 QY 252 GTCACTGGTCATATTATTTCCACCACAAATCGGTGGCAAAATGGTGAACCAAAACAGACA 311

DB 186 GTCACTGGCCACATAATCTCCACCACCTCGTGGTAAAAACGGAGAACCAAAAACAGACA 245  
 QY 312 ATTAGTTACATCGCGAGCGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTCCAGCA 371  
 DB 246 ATAAGTTACATCGCGAGCGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTCCAGCG 305  
 QY 372 AAATGTTGGAGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAAGATAC 431  
 DB 306 AAGTGTCTGGAGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAAGTAC 365  
 QY 432 AAGAACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGTGGTTGTTTGAAG 491  
 DB 366 AAGAACCGAGAGCTTCAGCTGATGCGTGTGATGATGAGCCATCCGAATGTGTTTGAAG 425  
 QY 492 CATTCGCTCTTTCGACTACAGAGAAAGACGAGCTTCTTGAACCTGGTGTATGGATAT 551  
 DB 426 CATTCGCTCTTTCGACCAAGAGACGAGCTGTTTCTGAACCTGGTGTATGGAGTAT 485  
 QY 552 GTCCCTGAGACGTTGTATCGAGTTCCTGAAACATTATAGTAGTGCAAAACCAAAAGATGCCT 611  
 DB 486 GTCCCTGAGAGCTTGTACCGAGTTCCTGAAACATTATACGACACTGCTTAACAGAGGATGCCG 545  
 QY 612 CTTGTCTATGTTAAACTTTACAGATTATCAGATCTTCCGGGACCTGCTTACATTCACAGT 671  
 DB 546 CTTGTCTATGTTAAACTCTATATGATACAGATCTTTCAGAGGACCTGCTTACATTCACAAAT 605  
 QY 672 TGCCCGGAGTTTGTACAGAGATCTTAAGCCTCAAAATCTTCTGGTTGATCCTCTTACT 731  
 DB 606 GTTGTGGAGTTTGTACAGAGATCTTAAGCCTCAAAATCTTCTGGTTGATCCTCTGACT 665  
 QY 732 CATCAAGTCAAAATCTGTGACTTTTGGCAGTGGCAAAACAGCTCGTTAAAGGTGAACCAAAAC 791  
 DB 666 CATCAAGTCAAGATCTGTGATTTTGGCAGTGGCAAAACAGCTTGTTPAAGGTGAAGCCAAC 725  
 QY 792 ATTTCTTACATCTGTCTACAGATTCTACCGTCAACCGAGCTCATATTTGGTGGCCTAGAG 851  
 DB 726 ATCTCTTACATATGTTCAAGATTCTACCGTCAACCTGAACTTATATTCGGTGGCCTAGAG 785  
 QY 852 TACACAACTTCTATTGATATCTGCTCTGCTGTGTTGTTCTTCTGCTGAGCTTCTTCTGCT 911  
 DB 786 TACACAACTTCTATTGATATTTGGTCTGCTGTGTTGTTCTCGCTGAGCTTCTTCTTGGT 845  
 QY 912 CAGCAATATTCCCGGAGAAAATCTGTGGATCAGCTCGTGGAAATTAATAAGTTCCTT 971  
 DB 846 CAGCCACTATTCTCTGGAGAAAATGCTGTGGGTGAGTCTGTTGAAATCATCAAAGTTCCT 905  
 QY 972 GTTACACCAACTCGAGAGAAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTC 1031  
 DB 906 GGTACACCAACTCGAGAGAGATCCGTTGTATGAATCCCACTACACAGACTTTAGGTTTC 965  
 QY 1032 CCACAGATAAAGGCCCATCCCTGGCACAAGATCTTCCACAAAGGATGCCCCAGAGCG 1091  
 DB 966 CCGCAGATAAAGGCACATCTTGGCACAAGATTTTCCACAAAGGATGCTTCCAGAGCC 1025  
 QY 1092 GTTGTATTTGGCATCAAGGCTGCTTCAATCTCTCAAAGTCTAAGATGCACAGCGCTCGAA 1151  
 DB 1026 ATTGATTTTGGCATCAAGGCTGCTTCAAGTCTTCAAGTCTTAGATGCACAGCGCTTGAA 1085  
 QY 1152 GCTTGTGACATCCGTTCTTGTATGAATCTCAGAGAACCAAAACGCTCGTTTACCAATGGA 1211  
 DB 1086 GCTTGTGACATCCGTTCTTGTATGAGCTTAGAGAACCAAAATGCTCGTTTACCAAAACGGA 1145  
 QY 1212 CGGCTCTCTCCGCTCTCTTCAACTTCAACAGAGTAGTGGATCATCACTGAGACTG 1271  
 DB 1146 CGGCTCTTCTCCGCGCTCTTCAACTTCAACAGAGTAGTGGAGCTTCACTGAGCTG 1205  
 QY 1272 GTCAACAAAGTGTGATTCAGACCATATCAAGAGACAAATGGGTCTAAGCTTCTTGAATCAA 1331  
 DB 1206 GTCAACAAAGTGTGATTCAGACCATATCAAGAGCGAGTGGTCTAAGCTTCTTGAATCAG 1265  
 QY 1332 TCTGGAACTTAAAGGGATCTCTGCAAAAGACAACTACTTTTATATATAA--TGTACCAT 1390









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QY 409 AGGTTTCAAGTAGACATACAGAACCGAGAACTTCAGTTGATGCGTGATGGATC 468
Db 342 AGGTTTCAAGACAGAGATACAGAAATCGTGAATACAGTTAAATGCGTGATGGATC 401
QY 469 ATCCGAATGTGTTGTTTGAAGACATGCTCTTTTCGAACTACAGAGAAAGACGAGCTTT 528
Db 402 ATCCAAATGTGATCTCTTTGAAGCATGTTCTTTCCACTACAGTACTGATGAATTT 461
QY 529 TCTTGAACCTTGTTATGGAGTAGTATGCCCTGAGACGTTGTTATCGAGTTCTGAACAATATA 588
Db 462 TTCTTAATTTGGTGTAGTAGTATGTTCCAGAGTCCATGTATAGAGTCTTAAAGCACTACA 521
QY 589 GTAGTGCAACCAAGAAATGCTCTGTTCTATGTTTAACTTTTACAGTTATCAGATCTTCC 648
Db 522 GCAATGCTAATCAAGAATGCTCTATCATCTAGTTTAACTTTTATATGTACCAAGATTTTCA 581
QY 649 GGGGAGCTTCTTACATTCACAGTTGCCCGGAGTTTGTCCAGAGATCTAAAGCCTCAA 708
Db 582 GGGGGTGGCTTATATCCACATGTTTCCCAAAGTTTGGCCAGAGATTTGAAGCCTCAA 641
QY 709 ATCTTCTGGTTGATCTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGGCAAC 768
Db 642 ATATATGTTGATCTCTTACACCAAGTGAAGCTATGTGACTTTTGAAGTGCAAAAG 701
QY 769 AGCTGTTAAAGGTGAACCAACATTTCTTACATCTGCTCAGATTTCTACGTCACCCG 828
Db 702 TTCTAGTCAAGGTGAAGCTAATATATCATATATGTTTACGGTTCTATCGAGACCAG 761
QY 829 AGCTCATATTTGGTGCACTGAGTACACAACTTCTATTGATATCTGCTGCTGTTGTG 888
Db 762 AACTCATATTTGGGGCCACAGAGTATCAAGTTCAATTTGATATTTGGTCAGTGGCTGTG 821
QY 889 TTCTTCTGAGCTTCTTCTTGTGTCAGCCATTTATCCCGGAGAAAATGCTGTGATCAGC 948
Db 822 TCCTTGTGAACTTCTTTTGGGCCAGCAATTTATCCCTGGCGAAAATGTCAGTAGACCAGC 881
QY 949 TCGTGAATTAATTAAGTTCTTGTGTACACCAACTCGAGAGAAATCCGTTGTATGAATC 1008
Db 882 TTGTACATATTAAGGTGCTTGGCACGCCCACTCGAGAGGAAGTACGCTGTATGAATC 941
QY 1009 CCAACTACACAGATTTCAAGTTTCCACAGATAAAGCCCATCCCTGGCACAGATCTTCC 1068
Db 942 CCAATTAATGACTTTAGTGTCTCAGATAAAGCACACCCATGGCCAAAGATATTCC 1001
QY 1069 ACAAAGGATGCCCCAGAGCGGTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAA 1128
Db 1002 ACAAAGAGTCTCGGAAGCTATTGATCTTGCATCCCGGCTGTTGCAATACTCCCAA 1061
QY 1129 GTCTAAGATGCAAGCGCTCGAAGCTTGTGCAATCCCGTTCTTGTATGAATCTCAGAGAAC 1188
Db 1062 GTCTCGGTGCACTGCACTTGAAGCATGTGCACATCTCTTCTTGTATGAATCTCGTGAAC 1121
QY 1189 CAAACGCTGTTTACCAATGACGCGCTCTCCGCTCTCTTCAACTTCAACACAGAG 1248
Db 1122 CCAACGCTCGCTGCCAAATGTCGCCCATTTTCCCTCTATTTAACTTCAACACAGAGAT 1181
QY 1249 TAGCTGGATCATCAGTCAACTGGTCAACAAGTTGATTTCCAGACCATATCAAGAGACAAAT 1308
Db 1182 TATCTGGACATCTCCGAGCTGTTTAAAGTTGATATCTGACCATCTGACCATGTGAAGCGGCAA 1241
QY 1309 TGGGTCTAAGCTTCTTGAATCAATCTGGAACTTAA 1343
Db 1242 TGGGGCTACAATTTATGCACTCTGGGAGGATCGTGA 1276
```

## RESULT 8

US-10-764-138-6

; Sequence 6, Application US/10764138

; Publication No. US20050081266A1

; GENERAL INFORMATION:

; APPLICANT: Sudwestdeutsche Saatzeucht-SWS

; APPLICANT: Advanta Seeds B.V.

; TITLE OF INVENTION: Modulation of Storage Organs

```
; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/10/764,138
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/09/578,194
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(1636)
; OTHER INFORMATION: strain Columbia ecotype
; OTHER INFORMATION: taxon:3702
; OTHER INFORMATION: tissue type leaves
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lechamy, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
; TITLE: from Arabidopsis thaliana ( Accession No. X94938, x94939 and X99696) ( PGR97-3)
; TITLE: (008)
; JOURNAL: Plant Physiol.
; VOLUME: 113
; ISSUE: 1
; PAGES: 306-306
; DATE: 1997-01-01
; DATABASE ACCESSION NUMBER: genbank/X94938
; DATABASE ENTRY DATE: 1998-02-13
; RELEVANT RESIDUES: (1)..(1636)
US-10-764-138-6
```

Query Match 42.3%; Score 734.6; DB 21; Length 1636;

Best Local Similarity 77.5%; Pred. No. 4.3e-201;

Matches 890; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

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QY 197 CGCATGCTGATGATAGTAAGGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCAC 256
Db 137 CGATATAGACAAACGACAGGAAATGCTGCTGCTGTTATAGAAAGGAAATGATGCTGTAC 196
QY 257 TGCTCATATTTTCCACCAATCGGTGGCAAAATGCTGAACCCAAACACACAAATTAG 316
Db 197 CGGTACACATATTTCTACTACATTTGGAGGCAAAATGTTGAACCTAAACAGACCATTAG 256
QY 317 TTACATGCGGAGCGAGTTGTTGTACAGGCTCGTTTCGGGATCGTTTCCAGCAAAATG 376
Db 257 TTACATGCGGAGCGAGTTGTTGTGGAACAGGATCATTCGGAATTTGTTCCAGGCAAAATG 316
QY 377 TTTGGAGACTGGAGAAACCGTGGCGGATAAAGAAGTTTTCGAAGATAGAAGATACAAGAA 436
Db 317 CTTGAAACTGGAGAACTCAGTAGCCATTAAGAAGTTTTCGAAGATCGCCGTTATAAAAA 376
QY 437 CGGAGAACTTCAGTTGATGCTGTGATGATCATCCGAATGCTGTTGTTGAAGCATTG 496
Db 377 CCGAGAGTTGCAATTAATTCGCACTAATGGAACCATCCAAATGTTGTTTCTTGAAGCATTG 436
QY 497 CTCTTTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCC 556
Db 437 TTTCTTCTACACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGTATGTACC 496
QY 557 TGAGAGCTTTGATCGAGTTCTGAACATTAATAGTAGTGCAAAACCAAGAAATGCCTCTTGT 616
Db 497 AGAGACATTTGACCGGGTTTGAAGCACTATACACTAGTTTCAAAACACGCGATGCTTATCT 556
QY 617 CTATGTTAACTTTTACAGTTATCAGATCTTCGGGGACTTCGTTACATTCACAGTTGCC 676
Db 557 CTATGTTAACTTTTACACATACCAAACTTCAGAGGCTTGGCTTATATCTACTACTGCTCC 616
QY 677 GGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTCTCTGGTTGATCTCTTACTCATCA 736
Db 617 TGGTGTCTGCCACAGAGATATAAACCAAAATCTTTTGGTTGATCTCCACACCCATCA 676
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Db	1236	TAGGCTCATCCAGAGCATATTAGGCGCGAGATGGGTCTCAGCTTCCGCGATCTTCGCGG	1295
Qy	1337	AACTTTAAAGGGATCTTCGAAAAGACAACACTACTTTTTTATATATAATGTACCATACACG	1396
Db	1296	TACATAGATGTAAGGGGATAATGAAACGATGAGTCAACCTACATAGTATGATCGATGTAAT	1355
Qy	1397	AGCCACAAGGTC	1408
Db	1356	CAACAGAAAGGC	1367

**RESULT 10**

```

US-10-424-599-67989
; Sequence 67989, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67989
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32407C.1
US-10-424-599-67989

```

[illegible]

Qy	666	CACAGTTGCCGGGAGTTTGTCTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCT	725
Db	587	CACACTGTTCCCAAAGTTTGGCCACAGAGACTTGAAGCCTCAAAATATACTGTGGTGGATCCT	646
Qy	726	CTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAA	785
Db	647	CTTACACCCAGTGAAGCTATGTGATTTTGGAAAGTGCAAAAGTTCTAGTAAAGGTGAA	706
Qy	786	CCAAACATTCTTTACATCTGCTCAGCATTTCTACCGTGCACCCGAGCTCATATTTGGTGCC	845
Db	707	GCTAAATATATCATACATATGTTTCAAGATTTCTATCGGCTCCAGAACTTATATTTGGCGCC	766
Qy	846	ACTGAGTACAACTTCTATTGATATCTGTCTGTCTGGTTGTGTTCTTGCTGAGCTTCTT	905
Db	767	ACAGAGTATCAAAAGTTCAATTTGATATTTGGCTAGCTGGCTGTGTCTTGTCTGAACTTCTT	826
Qy	906	CTTGGTCAGCCATTATTTCCCGCAGAGAAATGCTGTGGATCAGCTCGTGGAAATTTATTTAA	965
Db	827	TTGGGCCAGGCCATTATTTCTCTGGCG- AAATGCGATGAGACCAGCTTGGTCTATTTATAAG	885
Qy	966	GTTCCTTTGGTACACCAACTCGAGAGAAGAAATCCGTTGTATGAATCCCACTACACAGATTTC	1025
Db	886	GTGCTTTGGCACACCCACTCGAGAGGAAGTACGCTGTATGAATCCCAATTACAATGACTTT	945
Qy	1026	AAGTTCCACAGATAAAGGCCCATTCCTGTGCACAAAGATCTTCCACAAAAGGATGCCCCCA	1085
Db	946	AGGTTTCCACAGATAAAGCACACCCATGGCACAAAGATATTCACAAAAAGATGCTCTCCA	1005
Qy	1086	GAAGCGGTTGATTTGGCATCAAGGCTGCTTCATATCTTCCAGTCTTAAGATGCACAGCG	1145
Db	1006	GAAGCAATTGATCTTGATCCCGGCTTTTGGCAATATCTCCCAAGTCTCCGATGCACCTGC	1065
Qy	1146	CTCGAAGCTTGTGCACATCCGTTCTTTTGATGAACCTCAGAGAACCAAAACGCTCGTTTACCA	1205
Db	1066	CTTGAAGCATGTGCACATCTTTCTTTTGATGAACCTTCGAGAACCCATGCTCGCTGCCA	1125
Qy	1206	AATGGACGGCCTCTCCGCGCTCTCTTCAACTTCAAAACAAGAGTACGCTGATCATCACT	1265
Db	1126	AATGGTCGTCCATTCTCTCTTTTAACTTCAAGCAGGAATATTCGGAAGCTTCTCCA	1185
Qy	1266	GAACTGGTCAACAGTTGATTTCCAGACCATATCAAGAGACAATTGGGCTCTAAGCTTCTTG	1325
Db	1186	GAGCTTGTGAACAAAGTGATATCTGTACCACATGAAGCGGCAATAGGGCTGCAATTTGTT	1245
Qy	1326	AATCAATCTGGAACCTTAAAGGGATCTGCAAAAGACAACACTCTTTTATATATATATGT	1385
Db	1246	CGTCCGCGCAGGATCATGATGAAGCTTAGAGGGGGCATAGTGTACTAGTTGATNAAGT	1305
Qy	1386	ACCATTACACGACCCACAAGGTCGTAGTTGAA	1417
Db	1306	TAAACAAAAGTGGCCATTATTTTGTCTTAA	1337

## RESIT.T 11

US-10-424-599-124786  
 ; Sequence 124786, Application US/10424599  
 ; Publication No. US20040031072A1  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 124786  
 ; LENGTH: 2519  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max

FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_83691C.1  
US-10-424-599-124786

Query Match 39.8%; Score 688.2; DB 18; Length 2519;  
Best Local Similarity 76.5%; Pred. No. 1.5e-187;  
Matches 882; Conservative 0; Mismatches 268; Indels 3; Gaps 3;

QY 197 CGCCATGGCTGATGATAAGGAGATGCTGCTGCTGATGATGGACATGAT-CAAGTCA 255  
DB 783 CGATATGGAGACCGATAAGGATATGTCAGTCTCTGTCATTTGAGGGGAATGATGACGTTA 842

QY 256 CTGGTCATATTAATTTCCACCAATCGGTGGCAAAATGCTGAACCAAAACAGACAATTA 315  
DB 843 CTGGCCACATAATCTCCACCAATTTGGAGGCAAAATGGGAACCTTAACAGACCATCA 902

QY 316 GTTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTCCAGCAAAAT 375  
DB 903 GTTACATGGCAGAACGTTGTTGGCACTGGATCATTTGGAGTTGTTTCCAGGCAAAAT 962

QY 376 GTTTGGAGACTG-GAGAAACCGTGGCGATAAAGAAGGTTTTCGAAGATAGAGATACAG 434  
DB 963 GCTTGAGACTGCGAGAGGCGTGGCTATTAAGAGGCTTTGCAACAGCGGATACAA 1022

QY 435 AACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGCTGTTGTTGAAGCAT 494  
DB 1023 AATCGAGAAATTCAGTTAATGCGCTTAATGGATCACCAAACTAATCTACATGAAGCAC 1082

QY 495 TGGTCTCTTTTGGACTACAGAGAAAGA-CGAGCTTTTCTTGAATCTGGTATGGAGTATGT 553  
DB 1083 TTTTAAATTTCTCATCAAGCAAGATCCAACTTTTCTAAATCTGTTAATGAGATATGT 1142

QY 554 CCCTGAGAGCTGTATCGAGTCTGAAACATATAGTAGTGCAAAACCAAGATGCTCT 613  
DB 1143 CCCTGAGTCAATCAACCGAATTAATACCAATACACTACTATTAACAGAGATGCTCT 1202

QY 614 TGTCTATGTTAAACTTTACAGTTATCAGATCTTCCGGGACTTGTCTTACATTCACAGTTG 673  
DB 1203 CATCTACGTGAATCTGTATACATATCAATCTTCAGGGATTAGCATATATCCATCCGC 1262

QY 674 CCGGAGATTTGTCACAGAGATCTAAAGCTTCAAAATCTTCTGGTGTGATCTCTTACTCA 733  
DB 1263 CCTGCGAGTTTGGCATAGGATGTAAGCTTCAAAATCTTTTGGTTCATCTCTTACTCA 1322

QY 734 TCAAGTCAAAATCTGTGACTTTTGGCAGTGGCAACAGCTGTTAAAGGTGAACCAACAT 793  
DB 1323 CCAAGTTAGACTATGTATTTTGGGAGTCCAAAGTTCTGGTCAAGGTTGAATCAAAAT 1382

QY 794 TTCTTACATCTGCTCAGATTTACCGTGCACCGAGCTCATATTTGGTGCCACTGAGTA 853  
DB 1383 TTCATACATATGTTACAGTTACTATCGGGCTCCAGAACTAATATTTGGTGCACTGAATA 1442

QY 854 CACAACTTCTATTGATATCTGGTCTGCTGTTGTTCTTCTGGTGTGAGTCTTCTTGGTCA 913  
DB 1443 CACACCTTCTATTGATATCTGGTCACTGTTGTTCTTCTGCTGAACTTCTCTTAGGACA 1502

QY 914 GCCATTATTTCCCGGAGAAATCTGTGGATCAGCTCGTGGAAATTAATTAAGTCTCTGG 973  
DB 1503 GCCATTGTTTCTGGAGAAATCAGGTGGACCAACTTGTGGAAATTAATTAAGTCTCTGG 1562

QY 974 TACACAACTCGAGAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCC 1033  
DB 1563 TACTCCGACTCGGAGGAATCCGTTGCATGAACCCCAATTAACAGATTTAGATTTCCC 1622

QY 1034 ACAGATAAAGGCCCATCTCCGCAAGATCTTTCACAAAGGATGCCCCAGAGCGGT 1093  
DB 1623 TCAGATTAAGGCTCATCTTGGCACAAGGTTTTCACAAAGGATGCCCCAGAGCAAT 1682

QY 1094 TGAATTTGGCATCAAGGCTCTCAATCTCTCAAGTCTAAGATGCACGCGCTCGAAGC 1153  
DB 1683 TGACCTTGCATCAAGGCTCTCAATATTCACCTAGTCTACGCTGCACTCGCTGGAAGC 1742

QY 1154 TTGTGCACATCCGTTCTTTGATGAATCTCAGAGAACCAACGCTCGTTTACCAATGGACG 1213

DB 1743 ATGTGCACATCTTTCTTTGATGAGCTTCGCGAGCAAAATGCGCTCTCTCTAATGGCCA 1802

QY 1214 GCCTCTCCGGCTCTCTTCAACTTCAACAGAAAGTAGCTGATCATCACCTGAACTGGT 1273

DB 1803 TCCACTGGCCCCACATTTTCAACTTCAACAGAGAGTAGCTGGAGCATCACCTGAACTGAT 1862

QY 1274 CAACAAAGTTGATTTCCAGACCATATCAAGAGACAAATTTGGTCTTAAGCTTCTTGAATCAATC 1333

DB 1863 CAATAGGCTCATCCAGAGCATATTAAGCGGAGATGGTCTCAGCTTCCCGCATCTCTCG 1922

QY 1334 TCGAACTTAAAG 1346

DB 1923 CGGTTCATAGATG 1935

RESULT 12  
US-10-437-963-29872/c  
; Sequence 29872, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 29872  
; LENGTH: 1922  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_34331C.1  
US-10-437-963-29872

Query Match 39.4%; Score 685.4; DB 19; Length 1922;  
Best Local Similarity 75.5%; Pred. No. 8.2e-187;  
Matches 851; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

QY 224 TGCTGCTGATGATGGACATGATCAAGTCACTGCTCATATTTATTTCCACCAATTCGG 283

DB 1703 TGCTTCTTATGGAAGGAGTGTCTCTCAACCGGCCACATAATCTCCACACGATGG 1644

QY 284 TGGCAAAATGCTGACCAAAACAGACATTTAGTTACATGGCGGAGTGTGTTGGTAC 343

DB 1643 AGGGAAGAAATGAGAACCTTAAAGGACGATTAGCTACATGGCAGAACGAGTTGTGGGAAC 1584

QY 344 AGCTCGTTCCGGATCGTTTCCAAAGCAAAATGTTTGGAGACTGGAGAAACCGTGGCGAT 403

DB 1583 TGGATCATTTGAAATCGTCTTTCAGGCAAAATGTTTGGAGACTGGTGAAGCTGTGCCAT 1524

QY 404 AAAGAAGGTTTTCCAGATAGAGATACAAAGAACCGAGAACTTTCAGTTGATGCTGTGAT 463

DB 1523 TAAGAAGGTTTTACAGGACAAAGCGTTTACAAAGAACAGGAGATTGCAGATATATGCGATCAAT 1464

QY 464 GGATCATCGAATGGTTTGTGAGCATTTGTTGAGCATTTGTTTTCAGTACACAGAGAACGCA 523

DB 1463 GGATCATTCGAATGTTGTTTCTTTGAAGCATTTGCTTCTCTTACAAACAGAGAGATGA 1404

QY 524 GCTTTTCTTGAATCTGGTTATGAGATATGCTCCTGAGAGCTTGTATCGAGTCTCTGAAACA 583

DB 1403 ACTTTTCTTAACCTGCTCATGGAATTTGTTCTCTGAGTCACTGATCGTGTGTTGAAGCA 1344

QY 584 TTATAGTAGTGCAAACCAAGAAATGCTCTTGTCTATGTTAAACTTTACAGTTATCAGAT 643

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Db 1343 TTATAGCAACATGAACCAAGGATGCCACTTATATATATGTCAATTTGTATGTTTACCAGAT 1284
Qy 644 CTTCCGGGAGCTTGCTTACATTCACAGTTGCGCGGAGTTGTGTCAAGAGATCTAAAGCC 703
Db 1283 ATTCCGTGGTTTGGCTTTACATTCATCTAGCTGAGTTTGGCCACAGGATGTGAAGCC 1224
Qy 704 TCAAAATCTTCCTGGTTGATCTCTTACTCATCAAGTCAAAATCTGTGATTTGGCAGTGC 763
Db 1223 TCAGAAATCTTTGGTGGATGCTCTTACTCACAAGTCAAAATATGTGATTTTGGGAGCGC 1164
Qy 764 GAAACAGCTCGTTAAAGGTGAACCAAAATTTCTTACATCTGCTCACGATTTCTACCGTGC 823
Db 1163 AAAAAATGTTGTTAAAGGTGAACCAACATATCGTATATATGTTCAAGTTATTAACGTCG 1104
Qy 824 ACCGAGCTCATATTTGGTGGCCAGTACACAACTTCTATGATATCTGTCTGTGTCG 883
Db 1103 TCCAGAACTGATATTTGGGCAACCGAATACACGACATCAATGATATATGTCAGCTGG 1044
Qy 884 TTGCTGTTCTGCTGAGCTTCTTCTGGTCAGCATATTTCCCGGAGAAATGCTGTGA 943
Db 1043 GTGCTGTTCTGCTGAGTCTCTTCTGGCCAGCTCTCTTCTGCTGAAAGTGCAGTGA 984
Qy 944 TCAGCTCGTGGAAATTAATAAGTTCTTGGTACCAACTCGAGAAAGAAATCCGTTGTAT 1003
Db 983 TCAGCTGTTGCGATTAATAAGTTCTTGGTACTCCACACAGTGAAGAAATCCGCTGCAT 924
Qy 1004 GAATCCCACTACAGATTTCAAGTTCACAGATAAAGGCCCATCCCTGGCCACAAAGAT 1063
Db 923 GAATCCCACTACAGAAATTCAGATTTCTCAGATTAAGTCAACCCATGCCACAAAGAT 864
Qy 1064 CTTCCACAAAGGATGCCCCGAGAGCGTTGATTTGGCATCAAGCTGCTTCAATCTC 1123
Db 863 TTTCACACAGCGGATGCTTCCAGAGCAATTAACCTTGATCAGCTCTCTCCAGTATGC 804
Qy 1124 TCCAAAGTCTAAGATGACAGCGCTCGAAGCTTGTGCACATCGCTTCTTGTGATGAACCTCA 1183
Db 803 ACCAAATCTACAGTACAGCTGCTTCCAGAGCAATTAACCTTCTTGTGATGAATGGC 744
Qy 1184 AGAACCAACGCTCGTTTACCAATAGGAGCGCTCTCCGCTCTCTTCAACTTCAAAACA 1243
Db 743 AGAACCCACGCAAGGTTGCCAAATGGAGCTCCATTTCCCGCCACTGTTCAACTTAAAGCA 684
Qy 1244 AGAAGTAGCTGATCATCACTGAACTGCTCAAGTGTGATTCAGACCATATCAAGAG 1303
Db 683 AGAAGTAGCGAATATATCGCAGAGCTCATCAAGGTTGATACCAAGCATGCTCGCGC 624
Qy 1304 ACAATTTGGTCTAAGCTCTTCAATCAATCTCGAACTTAAAGGGAT 1350
Db 623 ACATTTGGGTTCAATTTCTTCCGCTGCTGCCGACCATAGGAGCGCT 577

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RESULT 13

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US-10-425-115-22950/c
; Sequence 22950, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22950
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_120933C.1
US-10-425-115-22950

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Query Match 39.0%; Score 678.4; DB 20; Length 1779;
Best Local Similarity 75.4%; Pred. No. 8.3e-185;
Matches 844; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy 223 CTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGTCAATATTTTCCACCAATCG 282
Db 1529 CTGGTCTATGATGAGGGAATGATCCAGTCAAGGTCATATATCTCAACACATG 1470
Qy 283 GTGGCAAAATTTGGTGAACCAAAACAGACAATTTAGTTACATGCGGAGCGAGTTGTGTA 342
Db 1469 GAGGGAAGATGGAGAGCTTAAAGACTATCAGCTACATGCGACAGAGAGTTGTGGGA 1410
Qy 343 CAGGCTCCTTGGGATCGTTTCCAGCAAAATGTTTGGAGACTGCGAGAAACCGTGGGA 402
Db 1409 CTGGATCATTCGGATCGTCTTCCAGGCAAAATGTTTGGAGACTGCTGAGACTGTTGCTA 1350
Qy 403 TAAAGAAGTGTTCGAAGATAGAAGATACAAAGACCGAGAACTTTCAGTTGATGCGTGA 462
Db 1349 TCAAGAAGTGTTCGAGGACAGCGCTACAAAGACAGGAGCTGCAAAATCATGCGATCCA 1290
Qy 463 TGGATCATCCGAATGTTGTTTGAAGCATTTGCTTCTTTTCGACTACAGAGAAAGAG 522
Db 1289 TGGATCATGCAATGCTGTTTCTTGAAGCATTTGTTCTTCTCCACACAGCAGAGATG 1230
Qy 523 AGCTTTCTTGAACCTTGGTATGAGATGTCCTCGAGAGCTGATCGAGTTCTGAAAC 582
Db 1229 AACTTTTCTTAACTTAGTGTGAGTTGTTCTCTGAGTCACTACATCGTGTCTGAAGC 1170
Qy 583 ATTATAGTAGTGAACCAAAAGAAATGCTCTGCTGATGTTTAAAGCTTTTACAGTTATCAGA 642
Db 1169 ACTACAGCAATATGAACAGAGAGATGCGCTTATTTATGTTAAATATATATACCTACCAGA 1110
Qy 643 TCTTCGGGAGCTTGTCTTACATTTACAGTTGCGCGGAGTTTGTTCACAGAGATCTAAAGC 702
Db 1109 TATTCGAGGTTAGCTTATATTCACAGATACCTGTTGTTGCCACAGGATGTGAAC 1050
Qy 703 CTCAAAATCTTCTGTTGATCTTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTG 762
Db 1049 CACAGAACTCTTTGGTTGATGCTTCACTCAAGTGAAGATATGTTATTTGGGAGTG 990
Qy 763 CGAAACAGCTGTTAAAGTGAACCAAAATTTCTTACATCTGCTCAGATTTCTACCGTG 822
Db 989 CAAAATGTTGGTCAAGGTTGAAGCAAAATTTATATATATATGCTCAGCTTATTAACCGTG 930
Qy 823 CACCGAGCTCATATTTGGTGCCTAGTACACAACTTCTTATGATATCTGCTGCTGCTG 882
Db 929 CTCCAGAGCTCATATTTGGGCAACCGAGTACACAACTCAATTTGTTGTTGCTGCTG 870
Qy 883 GTTGTGTTCTTGTGAGCTTCTTCTTGTGAGCCATTAATCCCGGAGAAATGCTGTGG 942
Db 869 GATGTGTTCTTGTGAGCTGCTTCTTGGCCAGCTCTCTTCCCTGGCGAAGTGTGTGG 810
Qy 943 ATCAGCTGTTGGAATTTAAAGTCTTGTGTACACCACTCGAGAGAAATCCCTGTA 1002
Db 809 ATCAACTTTGTTGAGATAATNAAGTTCTTGTGTCTCCAAACAGTGAAGAAATCCCGTTGA 750
Qy 1003 TGAATCCCAACTACACAGATTTCAAGTTTCCACAGATAAAGGCCCATCCCTGGCAAGA 1062
Db 749 TGAATCCCAACTACACAGATTTAGATTTCTCAGATCAAGCTCACCCATGGCACAGA 690
Qy 1063 TCTTCCACAAAGGATGCCCCCAGAGCGTTGATTTGGCATCAAGGCTGCTTCAATACT 1122
Db 689 TTTTCCACAAAGCGATGCTCCAGAGCTATAGATCTCGCTTACGTTTGTCTCCAGTACT 630
Qy 1123 CTCCAGTCTAAGATGACAGGCTCGAGCTTGTGCACTCCGTTCTTGTGATGAATCA 1182
Db 629 CACCAATCTAAGATGCACTGCTCTTGAAGCGTGTGCACTCCATCTTCTTGTAGTGTGC 570
Qy 1183 GAGAACCAAAAGCTGTTTACCAATGAGCGGCTCTCCCGCTCTCTTCAACTTCAAAAC 1242
Db 569 GAGAGCCACATGCGCGGTTGCCAAATGAGCGGCCAATTTCTCCACTGTTTCAACTTAAAC 510

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QY      1243   AGAAGTAGCTGGATCATCACTGAACTGGTCAACAAGTTGATTCCAGACCATATCAAGA   1302
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       509   AGGAAC TAGCAAATGCCCTCCCCGGAGTTCATCAACAGCGCTGATCCAGACCATGCTAGGC   450
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      1303   GACAAT TGGGTCTAAGCTTCTTGTAATCAATCTGGAACTTA   1342
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       449   GGCATCTTGGGCTCACTTTATGGCCACCGCTGGACCATA   410
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-425-114-32993
; Sequence 32993, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32993
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17050F06_FLI
US-10-425-114-32993

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Query Match	38.6%	Score 671.4	DB 18	Length 1887
Best Local Similarity	75.5%	Prod. No. 9.1e-183		
Matches 834	Conservative 0	Mismatches 271	Indels 0	Gaps 0
Qy	238	ATGACATGATCAAGTCTACTCGTCTATATTATTTCCACCACAAATCGGTGCGCAAAAATGGTG	297	
Db	178	AAGGGAGTGATCCGGTCAAGGTCAATATATCTCGAACCAATTCGAGGGAGAAATGGAG	237	
Qy	298	AACCAAAACAGACAAATTAGTTTACATGCGCGAGCGAGTTTGTGTGTCACAGCTCGTTTCGGGA	357	
Db	238	AGCCTAAAAGGACTATCAGCTACATGCGCAGAGAGAGTTTGTGGAACTCGATCAATTTGGAA	297	
Qy	358	TCGTTTTCCAAAGAAAATGTTTGGAGACTGGAGAGAAACCGTGGCGGATAAAGAAAGGTTTTGC	417	
Db	298	TCGTCCTCCAGGCAAAATGTCCTGGAGACTGGTGGAGACTGTTTCCGATTAAGAAGGTTTTGC	357	
Qy	418	AAGATAGAAGATACAAGAAACCGAGAACTTTCAGTTGATCGGTGTGATGATCATCCGAATG	477	
Db	358	AGGCAAGCGCTACAAGAAACAGGGAGCTACAATCATCGATCCATGGATCACTCCAAATG	417	
Qy	478	TGGTTTTGTTGAAGCATTTGCTTCTTTCCGACTACAGAGAAAGACGAGCTTTTCTTTGAAC	537	
Db	418	TTGTTTCTCTGAAGCATTTGCTTCTTCTCTACAAGCAGAGATGAACCTTTTCTTTAACT	477	
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; APPLICANT: VAN THIELEN, NOCHA			
; APPLICANT: DA COSTA E SILVA, OSWALDO			
; APPLICANT: CHEN, RUOYING			
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS			
; TITLE OF INVENTION: OF USE IN PLANTS			
; FILE REFERENCE: 16313-0178			
; CURRENT APPLICATION NUMBER: US/10/292,408			
; CURRENT FILING DATE: 2002-11-12			
; PRIOR APPLICATION NUMBER: 60/346,096			
; PRIOR FILING DATE: 2001-11-09			
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
7664.793 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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29	527.4	30.3	821	6	CB894470	EST647262	CB894470
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VERSION HTCC\_GSLT cDNA  
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SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 1409)  
AUTHORS Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Queirer, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.  
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1409)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length  
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 Hainey, C.P., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Design of Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
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 Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
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 Maize Mapping Project/DuPont Consensus Sequences for Design of  
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 Unpublished (2002)  
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 Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
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 assemblies resulting from the application of public  
 contigs to seed Dupont contigs; this resource was  
 assembled by DuPont as part of a collaboration for the

FEATURES  
 source

overgo addressing of BACs in conjunction with the Maize  
 Mapping Project\*  
 Query Match 36.5%; Score 634; DB 3; Length 1666;  
 Best Local Similarity 73.9%; Pred. No. 2.8e-156;  
 Matches 805; Conservative 0; Mismatches 285; Indels 0; Gaps 0;  
 QY 237 GATGGACATGATCAAGTCACCTGGTTCATATTTCCACCAAAATCGGTGGCAAAATCGT 296  
 Db 260 GAAGGGGAGAGCGCTGTGACGGGTACATCATCTCCACCATCGCGGGGAGAAACGGC 319  
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 Db 320 GAGCCCAAGCGGACCATCAGTTATCATGGCAGACGTCGTGGGTGACGGGCTCATTTGGG 379  
 QY 357 ATCGTTTCCAAAGCAAAATGTTTGGAGACTGCGAGAAACCGTGGCGATAAAGAGGTTTG 416  
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 QY 417 CAAGATAGAAGATACAAAGAACCGGAGAACTTCAGTTGATGCGTGTGATGGATCATCCGAAT 476  
 Db 440 CAGGATCGGCGTTACAAAGAACCGGAGCTGCAACTTATGCGTGCCATGAGCACCACCAAC 499  
 QY 477 GTGGTTTGTAAAGCATGCTCTTTTCGACTACAGAGAAAGAGAGCTTTTCTTGAAC 536  
 Db 500 GTCATCTGCTTGAAGCAGCTGCTTCTTCTCAACAGCAGCAGGAGCAGTGTGTTCTAAAC 559  
 QY 537 TTGGTTATGAGTATGTCCTGAGACGTTGATCGAGTTCTGAAACATTATATAGTAGTGA 596  
 Db 560 CTTGTGATGAAATTTGTCCTCCGAGACCTGTACCGTGTCTGAAAGCATACAGCAACGG 619  
 QY 597 AACCAAGAAATGCTCTTGTCTATGTTAAACTTTTACAGTTATCAGATCTTCGGGAGCT 656  
 Db 620 AACCAGAGGATGCTCTTATCTACGTCAGCTCAAGCTCTACATGATATCAGCTTTTCAGAGGCTA 679  
 QY 657 GCTTACATTCACAGTGGCCCGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTG 716  
 Db 680 GCCTATATTCAATATGATACCAAGGAGTCTGCCATAGGAGTGTAAAGCCCAAAACGTTTG 739  
 QY 717 GTTCATCTCTTACTCATCAAGTCAAATCTGTCAGCTTTGCGAGTCGCAAAACAGCTCGT 776  
 Db 740 GTTGATCTCTTACCCACAGCTCAAGCTCTGTGACTTGTAGGTCGCAAAAGTCTCTGATT 799  
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 Db 800 CCTGTGAACCGACATATCTTACATATGCTCTCGTTATTTATCGTCTCCAGAGCTCAT 859  
 QY 837 TTTGGTGCCTAGATACACAACTTCTATTGATATCTGCTGCTGCTGTTGTTGTTCTTCTGCT 896  
 Db 860 TTTGGAGCGACGAGTATACAACTTCAATAGACATATGCTCAGCTGGCTGTGTTCTAGCT 919  
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 Db 920 GAGTTGCTTCTTGTGTCAGCACTGTTCGCGGAGAGAGTGTGTTGATCAGTTGATGAG 979  
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 QY 1197 CGTTTACAAATGAGCGGCTCTCTCCGCTCTCTCTTCAACTTCAAAACAGAAAGTAGTCTGA 1256



Library" this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

## ORIGIN

Query Match 35.9%; Score 623.4; DB 3; Length 1967;  
Best Local Similarity 73.4%; Pred. No. 1.9e-153;  
Matches 811; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

207	QY	GATGATTAAGGAGATGCCTGCTGCTGTAGTTGATGGCAATGATCAAGTCACTGCGTCATATT	266
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516	Db	ATTGTCACCACTACTGGTGGCAAGAATGGTCAACAAACAGACAGTAGGAGCTACTATGGCT	575
327	QY	GAGCGAGTTGTTGTTACAGGCTCGTTTCGGGATCGTTTTTCCAAAGCAAAATGTTTGGAGACT	386
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387	QY	GGAGAAACCGTGGCGATAAAGAAAGTTTTGCAAGATAGAAATCAAGAAACCGAGAACTT	446
636	Db	GGTGAGACTGTGTCATAAAGAAAGTTCTTCAAGACAAAGCTTTACAAGAACCGCGAACTG	695
447	QY	CAGTTGATGGTGTGATGGATCATCCGAATGTGGTTTTGTTTGAAGCATTTGCTCTTTTCG	506
696	Db	CAGACCAATGCGCCTTCTTGACACCCTTAATGTTGTGCTTTTGAAGCATTTGCTCTTTTCA	755
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756	Db	ACTACTGAGAAGATGATGACTTTATCTGAATTTGTTGCTTGGATGATGTTCCGAGACAGATT	815
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816	Db	CATCGAGTTGTGAAACATCAACAAGATGCACCACGCACTGCCACTATTTATGTGAAG	875
627	QY	CTTTACAGTTATCAGATCTTCCGGGAGCTTGCTTTACATTTACAGTTGCCCGGGAGTTTGT	686
876	Db	CTTTTATATGTAACAGATATGTAGAGCATTTGGCTTTACATTTCACTGCTGTACTATCGGTGTCTGC	935
687	QY	CACAGAGATCTAAGACCTCAAAATCTTCTGTTGATCTCTTACTCATCAAGTCAAAATC	746
936	Db	CACAGAGATTAATAGCCACAAATCTTCTGTTGAACCCACACCCACAGCTTTAAATA	995
747	QY	TGTGACTTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAACCAAAACATTTCTTACATCTGC	806
996	Db	TGTGACTTTTGTAGTCAAAAGTTCTGTTCAAGGGGNAACCAACATATCATACATCTGC	1055
807	QY	TCACGATTTACCGTGCACCCGAGCTCATATTTGGTGCACCTGAGTACACAATTTCTATT	866
1056	Db	TCGCGATACTATAGGGTCCAGAGCTCATATTTGGTGCACCTGAGTATACCACAGCGATT	1115
867	QY	GATATCTGGTCTGCTGTTGTTCTTGCTGAGCTTCTTCTGCTCAGCCATTAATTTCCCG	926
1116	Db	GACATTTGGTCTGCTGATGTTTCTTGCTGAGCTTATGCTAGGGCAGCCCTTGTGTTCCG	1175
927	QY	GGAGAAATGCTGTGGATCAGCTCGTGGAAATTAATAAGTTCTTGCTACACCAACTCGA	986
1176	Db	GGTGAAGTGGTGGACCAACTGTTTGAATCATCAGGTCTTCGGTACGCCAACAGG	1235
987	QY	GAAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTTCCACAGATAAAGGCC	1046
1236	Db	GAAGAAATTAATGTCATGAACCCAAATTAACACAGAGTTTAAGTTTCCACAAATCAAAGCA	1295
1047	QY	CATCCCTGGCAAGATCTTCCACAAAGGATGCCCGCCAGAGCGGTTGATTTGGCATCA	1106
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Query Match 35.2%; Score 611.8; DB 3; Length 1638;  
Best Local Similarity 72.5%; Pred. No. 2.1e-150;

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Qy	1167	TTCCTTTGATGAACCTCACAGAACCAAACGCTCGTTTACCAAATGGACGGCCTCTCCCGCCT	1226
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Qy	1227	CTCTTCAACTTCAA ---ACAAGAAGTAGCTGGATCATCACCTGAACCTGGTCAACAAGTTG	1283
Db	1476	CTATTCAATTTCAAGCCTCAGCACTTAAGGAGTCCCATCAGACATGTTGGCAAAATTG	1535
Qy	1284	ATTCACAGACCATTACAAGACAAAT	1308
Db	1536	GTTCCAGAAATGCGAAGAAGCAAT	1560

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LOCUS	CNS09YSF      1638 bp    mRNA    linear    HTC    06-FEB-2004
DEFINITION	Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSUTLS91ZE05 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION	BX831446
VERSION	BX831446.1 GI:42455013
KEYWORDS	HTC; GSLT cDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
1 (bases 1 to 1638)  
AUTHORS  
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,  
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,  
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
TITLE  
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome

**JOURNAL  
REFERENCE**  
2 (bases 1 to 1638)  
**Annotation**  
Unpublished

**AUTHORS**  
**TITLE**  
**JOURNAL**  
**Genoscope. Centre National de Sequences : Direct Submission**  
**Submitted (18-NOV-2003)**  
**BP 191 91006 EVRY cedex - FRANCE (E-mail : sequest@genoscope.cns.fr)**  
**- web : www.genoscope.cns.fr)**

COMMENT

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted June 1, 2013. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

<http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis>.  
 Location/Qualifiers  
 source : 1..1638

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ORIGIN

Query Match 35.2%; Score 611.8; DB 3; Length 1638;  
Best Local Similarity 72.5%; Pred. No. 2.1e-150;







Db	327	GAACCTTAAAGGGATCCTGCAAAAGACAACTATCTTTTATATATAATGATACCAATTACAC	268
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Db	267	GAGCCACAAAGTCCGTAGTTGAAGGCAACCGTGGAGGACACAATTTCAAAGTTTTTTCCTCCT	208
Qy	1456	CAAACTCGTTTCAGACAAAGCCAGCTGCTAGCAAAACCAACT-ACCCAAATCTGCGAAAAC	1514
Db	207	CAAACTCGTTTCAGACAAAGCCAGCTGCTAGCAAAACCAACTCCTCCCAACTCTGCGAAAAC	148
Qy	1515	AAAACTCTCCAGTGTGTATCTGCTATTATTTCTCTCTTTTCAAGTTCCTGGTGAAAAAC	1574
Db	147	AAAACTCTCCAGTGTGTATCTGCTATTATTTCTCTCTTTTCAAGTTCCTGGTGAAAAAC	88
Qy	1575	ACAGTCTCCTCTTTCGCTTCATTTCTTTTCTTTTCCCTTATGTAATCAGTTTAGTCA	1634
Db	87	ACAGTCTCCTCTTTCGCTTCATTTCTTTTCTTTTCCCTTATGTAATCAGTTTAGTCA	28
Qy	1635	GAAGTTTTTTTATATAGTAAAGTTTGG	1661
Db	27	GAAGTTTTTTTATATAGTAAAGTTTGG	1
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LOCUS			
DEFINITION			
CA781809 Infected Arabidopsis Leaf mRNA linear EST 03-DEC-2002			
sequence.			
CA781809			
CA781809.1 GI:26019845			
EST.			
Arabidopsis thaliana (thale cress)			
Arabidopsis thaliana			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi			
1 (bases 1 to 665)			
REFERENCE			
AUTHORS			
Lundegaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.			
and Welinder,K.G.			
TITLE			
EST sequencing of Erysiphe cichoracearum infected Arabidopsis			
plants			
JOURNAL			
COMMENT			
Unpublished (2002)			
Contact: Karen G. Welinder			
Institut for bioteknologi			
Aalborg Universitet			
Sohnegaardsholmsvej 49, 9000 Aalborg, Denmark			
Tel: +45 96358467			
Fax: +45 98141808			
Email: kgw@bio.auc.dk.			
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/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA			
library of Arabidopsis and E. cichoracearum infected leaf			
from three weeks old Arabidopsis plants. Plants were			
harvested 3 days after infection and mRNA oligo dt			
selected."			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 638; Conservative 0; Mismatches 26; Indels 2; Gaps 2;			
373 AATGTTGGAGACTGGAGAAACCTGGCGATATAAGAGGTTTTTCAAGATAGAAGATACA			
432			
Db			
1 AATGTTGGAGACTGGAGAAACCTGGCGAT-AGAAGGTTTTTCAAGATAGAAGATACA			
59			
Qy			
433 AGAACCGAGAACTTCAGTTGATCGTGTGATGATCATCCGAATGTGGTTTGTGGAAC			
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QY	189	GTCTCTATCCCATGCTGATGATAGGAGATCCCTGCTGCTGTAGTGTGACATGAT	248
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QY	309	ACAATTAGTTACATGCGGAGCGAGTTGTTGTACAGGCTCGTTCGGGATCGTTTTCCAA	368
Db	379	ACCAATTAGTTACATGCTGAGCGGTGTAGTGTATGCTTCCGAAACCGTTTTCCAG	438
QY	369	GCAAAATGTTGAGACTGAGAAACCGTGGCATAAAGAGTTTTCGAAAGTACAGTAAGA	428
Db	439	GCCAAGTGTCTTGAATCTGTGAGCGGTAGCTATATAAAAGGTTCTTCAAGACAAGAG	498
QY	429	TACAAGAACCGAGAACTTCAGTTGATGCTGATGATCATCCGATGTTGTTGTTG	488
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QY	489	AAGCATTGCTCTTTTCGACTACAGAGAAAGACGAGCTTTCTTGAACCTTGTGTATGGAG	548
Db	559	AAGCAGCTGTTTCTTCTCAAGACTGAGAAAGAGAGCTTTTACCTCAATTTGGTGTGAG	618
QY	549	TATGTCCTGAGAGTTGTTATCGAGTTCTGAAACATATAGTAGTGAACCAAGAAATG	608
Db	619	TATGTACCGGAGACTGCTCATCTGTGTATCAAAACATTTACAAAGATGAACCAAGCGCATG	678
QY	609	CCTCTTGTCTATGTTAACTTTACAGTTATCAGATCTTCGGGGACTTGTCTTACATTTCAC	668
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QY	669	AGTTGCCCGGAGTTTGTCAAGAGATCTAAAGCCTCAAAATCTTCTGTTGTGATCTCTTT	728
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QY	729	ACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGGCAACAGCTCGTTAAAGGTGAACCA	788
Db	799	ACCCATCAGCTAAATTTGTGTGACTTTGGCAGCGCGGAAAGTTCTGGTAAAGGCGAACCA	858
QY	789	AACATTTCTTACATCTGCTCAGCATTTACCGTGCAACCGAGCTCATATTTGGTGGCACT	848
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QY	849	GAGTACACAACTTCTATTTGATATCTGGTCTGCTGGTTGTCTTCTGCTGAGCTTCTTCTT	908
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QY	909	GGTGAGCATATTTCCCGGAGAAATGCTGTGATCAGCTCTGTGGAAATTTATAAGTT	968
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QY	969	CTTGTGTACACCAACTCGAGAGAAATCCCTGTATGAATCCCAACTACACAGATTTCAAG	1028
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QY	1029	TTCCACAGATAAAGGCCCATCCCTGGCAAGATCTTCCAAAAAGGATGCCCCAGAA	1088
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Db	1159	GGGTTGATTTCTCGTGTCCAGGCTTTCGAGTACTACCAAAACTTCGGTGCAGTGTCTTG	1218
QY	1149	GAACTTGTGCACATCCGTTCTTTGATGAACCTCAGAGAACCAACGCTCGTTTACCAAT	1208
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QY	1209	GGACGGCTCTCCCGCTCTCTTCAACTTCAAC	1242
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<p>RESULT 12</p>			
<p>CNSOADOL</p>			
<p>LOCUS</p>			
<p>DEFINITION</p>			
<p>Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB37ZG06 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).</p>			
<p>ACCESSION</p>			
<p>VERSION</p>			
<p>KEYWORDS</p>			
<p>SOURCE</p>			
<p>ORGANISM</p>			
<p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.</p>			
<p>1 (bases 1 to 1870)</p>			
<p>Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.</p>			
<p>Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation</p>			
<p>Unpublished</p>			
<p>2 (bases 1 to 1870)</p>			
<p>Genoscope.</p>			
<p>Direct Submission</p>			
<p>Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)</p>			
<p>The sequences are based on single pass reads.</p>			
<p>Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.</p>			
<p>Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.</p>			
<p>URV INRA : Clepet C., Caboche M.</p>			
<p>Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.</p>			
<p>http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length</p>			
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**Matches 782; Conservative 0; Mismatches 306; Indels 3; Gaps 1;**

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Db	96	GTCCGCGGAGGAAGCATGGTCCCACTATAATGGGAGAAATGATCCAGTCACAGGTCA	155
Qy	263	TATTATTTCCACCACCAATCGTGGCCAAAATGCTGGAACCAAAACAGACAAATTAGTTACAT	322
Db	156	TATAAATTTCACTACTATTGGAGGAAGACGATGAGCCCAAAGGACTATTAGCTATAT	215
Qy	323	GGCGGAGCGAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTCCAAAGCAAAATGTTTGA	382
Db	216	GGCTGAACGAGTTGTTGGAACCTGGATCCTTGGTGTGATTCCAGGCAAAATGCTTGA	275
Qy	383	GACTGAGAGAAACCGTGGCGGATAAAGAAGTTTTCGAAGATAGAAGATACAAGAACCGAGA	442
Db	276	GACTGGTGAACCTGTTGGCCATTAAAGAAGTCTTACAGGACAAACGATACAAGAACAGAGA	335
Qy	443	ACTTCAGTTGATCGGTGTGATGATCATCCGATGTGGTTTGTTCGAGCATTCGCTTC	502
Db	336	GTTTACAGATAATCGGATCAATGGATCATTCGCAATGCATCTCCCTAAAGCATTTGTTCTT	395
Qy	503	TTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAAGTATGTCCTCCCTGAGAC	562



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Db      422  CAGTATAGAGTTTGAAGCAATACAGCAGTGCAGATCGAAATCAGAGATGCCCTCATATATGT 481
Qy      623  TAAACTTTACAGTATACAGATCTTCGGGGAGCTTGCTTACATTCACAGTTGCCGGGAGT 682
Db      482  GAAACITTTATACGTACAGATTTTCAGGGGCTGGCTTACATCCACACATGTTCTCGAGT 541
Qy      683  TTGTACAGAGATCTAAAGCTCAAAATCTTCGGTTGATCTCTTACTCATCAAGTCAA 742
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Qy      743  AATCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAACCAACATTTCTTACAT 802
Db      602  GATTTGTGATTTTGAAGTGCAGAACAGCTGATTCGTGGAGAGCAACATATCATACAT 661
Qy      803  CTGCTCACGATTTCTACCGTGCACCCGAGCTCATATTTGGTGGCACTTGAGTACACAACTTC 862
Db      662  ATGTTACAGTTCTTATCGGCTCGGAACCTATATTTGGAGCTACAGATATACAACTTC 721
Qy      863  TATGTATATCTGCTGCTGTTGTTGTTCTGCTGAGCTTCTTCTGTCAGCCATTTATT 922
Db      722  AATTGATATATGTCAGCTGGTTGTGCTTGCAGCTTCTTTGGGCGAGCCATTTATT 781
Qy      923  CCCCAGAGAAATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 982
Db      782  TCTGTGAGAAATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
Qy      983  TCGAGAGAAATCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1028
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## RESULT 15

CK266410  
 LOCUS EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA  
 DEFINITION clone POAC457 5' end, mRNA sequence.

CK266410  
 VERSION 1  
 KEYWORDS

SOURCE Solanum tuberosum (potato)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Solanum.  
 1 (bases 1 to 924)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

Unpublished (2003)

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Email: potato-array@igr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

## FEATURES

source  
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 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
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 /clone="POAC457"  
 /tissue\_type="abiotic stress treated leaf and root tissue"  
 /lab\_host="PH108-Tona"  
 /clone\_lib="potato abiotic stress cDNA library"  
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;  
 supplier: Solanum tuberosum var. Kennebec plants were  
 grown from cuttings on a 16hr light/8 hr dark cycle at 25  
 C for 3-4 weeks. Abiotic stress conditions were applied to  
 four separate sets of plants. Set 1 involved saturation of  
 the soil with 150 mM NaCl and tissues were harvested at  
 following application of the salt stress (leaves: 2hr,

6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).  
 Set 2 were grown under the standard conditions and then  
 were water stressed by withdrawal of further watering  
 applications. Drought stressed plants were harvested after  
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d  
 and 5d). Set 3 were grown under the standard conditions  
 and then were cold stressed by placement at 4 C. Cold  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d. Set 4 were grown under the standard conditions and  
 then were heat stressed by placement at 35 C. Heat  
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,  
 2d and 4d and heat-stressed roots were harvested at 6 hr,  
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and  
 equal RNA from each tissue and stress was pooled to  
 construct the cDNA library. RNA sample."

## ORIGIN

Query Match 33.4%; Score 579.8; DB 7; Length 924;  
 Best Local Similarity 76.9%; Pred. No. 5.5e-142;  
 Matches 707; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

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Qy      346  GCTCGTTCGGGATCGTTTCCAAAGCAAAATGTTTCGAGACTGGAGAAACCGTGGCGATAA 405
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Db      61  AGAAGGTTTTCAGGACAGCGGTATATAAACCGTGAACACTACAACATGATGCGCTTGTATGG 120
Qy      466  ATCATCCGAATGTGGTTGTTGAAGCAATGCTTCTTTTCGACTACAGAGAAAGACGAGC 525
Db      121  ATCACCAGAAATGTCTATTACTCTTAAAGCACTGCTTCTTTTCCACGACTAGTAGAGATGAGC 180
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Db      301  TCAGAGGGCTGGCTTACATTCATATGTTTCCAAGAAATTTGCCATAGAGATGTGAAACCTTC 360
Qy      706  AAAATCTTCTGGTTGATCTCTTACTCATCAAGTCAGTCAAAATCTGTCACTTTGCGAGTGGCA 765
Db      361  AAAATCTTGGTTGATCTCTGACCCATCAAGTCAAGTATGTGATTTTGAAGTGCAGAA 420
Qy      766  AACAGCTGTTAAAGGTGAACCAAAACATTTCTTACATCTGCTCAGGATTTCTACCGTGCACT 825
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QY      1246  AAGTAGCTGGATCATCACC 1264
Db      901  AGTTAACTGGAGCTTCACC 919

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Search completed: June 24, 2005, 06:43:11  
Job time : 8635.11 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 11439.2 Seconds  
(without alignments)  
6929.914 Million cell updates/sec

Title: X94938  
Perfect score: 1636  
Sequence: 1 TTTACTCTTCAGTCAGAGA.....AAAAAAAAAAAAAAAAAAAA 1636

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_hg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	100.0	1636	8	ATASKDZET
2	1546.4	94.5	1591	8	X94938 A.thaliana
3	1537.8	94.0	1566	8	AY094423 Arabidops
4	1478	90.3	1503	8	AY064020 Arabidops
5	1263.6	77.2	1270	8	AY087542 Arabidops
6	975.6	59.6	1572	8	AY096698 Arabidops
7	974.2	59.5	1582	8	AF019927 Arabidops
8	972.2	59.4	1614	8	AY035048 Arabidops
9	939.8	57.4	1255	8	X99696 A.thaliana
10	734.6	44.9	1738	8	AY051053 Arabidops
11	733	44.8	1636	8	X94939 A.thaliana
12	731.4	44.7	1670	8	AY086529 Arabidops
13	730.8	44.7	1143	6	AY075699 Arabidops
14	730.8	44.7	1143	6	CQ804868 Sequence
15	694	42.4	2055	8	AX506180 Sequence
16	662.8	40.5	1825	8	AK073725 Oryza sat
17	662.8	40.5	1863	8	AK100950 Oryza sat
18	661.2	40.4	1818	8	AK102147 Oryza sat
19	660.4	40.4	1744	8	BT009253 Triticum

20	659.6	40.3	1797	8	OSKETHA
21	616.6	37.7	1233	8	BT010466 Arabidops
22	616.6	37.7	1712	8	AY065043 Arabidops
23	609.8	37.3	1581	8	PHPSK4
24	605.2	37.0	2030	8	AY339067 Physomit
25	602.2	36.8	1249	8	AY142595 Arabidops
26	602.2	36.8	1634	8	AF428327 Arabidops
27	602.2	36.8	1667	8	AY046024 Arabidops
28	599	36.6	1724	8	NTNTKLRN
29	594.2	36.3	1496	8	ATASKA
30	594.2	36.3	1496	8	ATRNAASKA
31	593.6	36.3	1613	8	AMMSKIA
32	591	36.1	1717	8	AY085752 Arabidops
33	588.4	36.0	2092	8	NTNSK6
34	588	35.9	1658	8	ATRNAASKG
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36	587.8	35.9	1401	8	AY093347 Arabidops
37	587.8	35.9	1630	8	AY062713 Arabidops
38	584.2	35.7	1592	8	AB059621 Oryza sat
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43	580.6	35.5	2136	8	AK072390 Oryza sat
44	579.2	35.4	1859	8	AY339066 Physomit
45	573.8	35.1	1543	8	AMMSK2A

## ALIGNMENTS

RESULT 1	ATASKDZET	1636 bp	mRNA	linear	PLN 13-FEB-1998
LOCUS	A.thaliana mRNA for shaggy-like kinase dzeta.				
DEFINITION	X94938.1 GI:1161509				
ACCESSION	ASK dzeta gene; serine/threonine kinase; shaggy-like kinase dzeta.				
VERSION	Arabidopsis thaliana (thale cress)				
SOURCE	Arabidopsis thaliana				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.				
REFERENCE	1				
AUTHORS	Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.				
TITLE	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)				
JOURNAL	Plant Physiol. 113, 306-306 (1997)				
REFERENCE	2 (bases 1 to 1636)				
AUTHORS	Dornelas,M.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE				
COMMENT	Corresponding genomic sequence: Y09300.				
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		Best Local Similarity 100.0%; Pred. No. 1.2e-294;			
		Matches 1636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	61	TGGGGCTCTCTCAGCCCTCGTCTTTAGCTCCTCAGCGCGCGATCTTCACGGCGGAGATT	120	841	TACTTCTTTGGGAGAGCGGTATTCCCGGAGAGAAATTCGTGGACACAGCTAGTGGAGATCA
DB	61	TGGGGCTCTCTCAGCCCTCGTCTTTAGCTCCTCAGCGCGCGATCTTCACGGCGGAGATT	120	901	TAAAGGTTCTTGCTACTCCAACTCCCGAAGAAATCCGGTGCATGAACCCAAACTACACAG
QY	121	CTTTGAAACGTCCTCCGATATAGACAACGACAGGAATGTCTGCTGTATTAGAAG	180	901	TAAAGGTTCTTGCTACTCCAACTCCCGAAGAAATCCGGTGCATGAACCCAAACTACACAG
DB	121	CTTTGAAACGTCCTCCGATATAGACAACGACAGGAATGTCTGCTGTATTAGAAG	180	961	ACTTCAGATTCCCACAAAATCAAAGCCACCTTGGCATAAAGGTTTTTCCACAAGCGGATGC
QY	181	GAAATCATCTGTACCGTGCATATATTTCTACTACATTTGGAGCAAAATGGTGAAC	240	1021	CTCCGGAAGCATTTGACCTTGCATCTCGGCTTCTTCAATACTCACCAGTCTACGTTGCA
DB	181	GAAATCATCTGTACCGTGCATATATTTCTACTACATTTGGAGCAAAATGGTGAAC	240	1021	CTCCGGAAGCATTTGACCTTGCATCTCGGCTTCTTCAATACTCACCAGTCTACGTTGCA
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DB	241	CTAAACAGACCATTAGTTATCATGGCCGACGCTGTGTGGAAACAGGATCATTCGGAATTG	300	1081	CTGGCTCGAGCATGTGGCATCCGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTC
QY	301	TATTCAGGCAAAATCGTTGGAATCGGAGATCAGTAGCCATTAAGAAGTTTTCGAAG	360	1141	TTCCAAATGGCGGACCTCTACCAACGTTTGTCAAACTTCAAAACAAGATTGTCTGGGGCTT
DB	301	TATTCAGGCAAAATCGTTGGAATCGGAGATCAGTAGCCATTAAGAAGTTTTCGAAG	360	1141	TTCCAAATGGCGGACCTCTACCAACGTTTGTCAAACTTCAAAACAAGATTGTCTGGGGCTT
QY	361	ATCGCGTTTATAAAACCGAGAGTTCGAATTAATGCGACTAATGGACCATCCAAATGTGG	420	1201	GACCGAGCTTATCAACAGGCTTAATACAGAGCATGTGAGGCGACAGATGAATGGTGC
DB	361	ATCGCGTTTATAAAACCGAGAGTTCGAATTAATGCGACTAATGGACCATCCAAATGTGG	420	1201	GACCGAGCTTATCAACAGGCTTAATACAGAGCATGTGAGGCGACAGATGAATGGTGC
QY	421	TTTCTTGAAGCATTTGTTCTCTACAAACGACTAGAGATGAGCTCTTCTCAATCTCG	480	1261	TTCCATTTCAAGCTGGACCCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGCAAAATGC
DB	421	TTTCTTGAAGCATTTGTTCTCTACAAACGACTAGAGATGAGCTCTTCTCAATCTCG	480	1261	TTCCATTTCAAGCTGGACCCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGCAAAATGC
QY	481	TTATGAGTATGACACAGACATTTGACCGGTTTGAAGCACTATACCTAGTTCAAAAC	540	1321	CGCTTATGGAAATGAAGGAGCGGAGATTACTTCTCTGATTAACCTAAGTATCAGCTT
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QY	541	ACGGGATGCTATCTTCTATGTCAAACTTTACACATACCATACTTCAGAGGCTGGCTT	600	1381	CTGAGAAGAGATGATGTCCTCTTAGACGGCCCAATTCAGCTTTTGGAGAAATCAGG
DB	541	ACGGGATGCTATCTTCTATGTCAAACTTTACACATACCATACTTCAGAGGCTGGCTT	600	1381	CTGAGAAGAGATGATGTCCTCTTAGACGGCCCAATTCAGCTTTTGGAGAAATCAGG
QY	601	ATATCCATCTGCTCTGCTGTGCTGACAGATATAAACACACAAATCTTTTGGTTG	660	1441	AGCGGATGATCTGTCCTCAATTAATCTTTTGTTCACCTGACTTGTAGAGAGATCTTTT
DB	601	ATATCCATCTGCTCTGCTGTGCTGACAGATATAAACACACAAATCTTTTGGTTG	660	1441	AGCGGATGATCTGTCCTCAATTAATCTTTTGTTCACCTGACTTGTAGAGAGATCTTTT
QY	661	ATCCCAACCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGGTGAAG	720	1501	CTCCTGTATCAGTATTTGATATGTTTTTGTCTTGAATGAAACAAAAATCGATTCCAAA
DB	661	ATCCCAACCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGGTGAAG	720	1501	CTCCTGTATCAGTATTTGATATGTTTTTGTCTTGAATGAAACAAAAATCGATTCCAAA
QY	721	GTGAACCAACATATCATATCTGCTCGGTATTACCGAGCTCCAGAACTCATCTTTG	780	1561	AAAAAAA
DB	721	GTGAACCAACATATCATATCTGCTCGGTATTACCGAGCTCCAGAACTCATCTTTG	780	1561	AAAAAAA
QY	781	GTGCCACAGAGTATACATCATCATATGATATGCTGCTGTTGTCTGCGAGAGC	840	1621	AAAAAAA
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		DEFINITION			
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		ACCESSION			
		AY094423.1			
		VERSION			
		GI:20453107			
		KEYWORDS			
		FLI CDNA.			
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		Arabidopsis thaliana (thale cress)			
		ORGANISM			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
		rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.			
		REFERENCE			
		1 (bases 1 to 1591)			



AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	61	TTGGGCTCTCTCAGCTCCGCTCTTTAGTCTCTCAGCCCGCATCTTCAACGGCGAGATT	120
	Arabidopsis cDNA clones	Db	96	TTGGGCTCTCTCAGCTCCGCTCTTTAGTCTCTCAGCCCGCATCTTCAACGGCGAGATT	155
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	121	CTTTGAAACGTCGTCGGATATAGACAACGAAATGTCTGCTCTGTATTATAGAAG	180
	Arabidopsis cDNA clones	Db	156	CTTTGAAACGTCGTCGGATATAGACAACGAAATGTCTGCTCTGTATTATAGAAG	215
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	181	GAATGATGCTGTTTACCGGTACATAAATTTCTACTACAAATGGAGGCAAAAATGGTGAAC	240
	Arabidopsis cDNA clones	Db	216	GAATGATGCTGTTTACCGGTACATAAATTTCTACTACAAATGGAGGCAAAAATGGTGAAC	275
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	241	CTAAACAGACCATTTAGTTACATGCGCGAAAGTGTGTTGGAAACAGAGATCATTTGGAATTTG	300
	Arabidopsis cDNA clones	Db	276	CTAAACAGACCATTTAGTTACATGCGCGAAAGTGTGTTGGAAACAGAGATCATTTGGAATTTG	335
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	301	TATTCACGAGCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAAAGGTTTTCGAAG	360
	Arabidopsis cDNA clones	Db	336	TATTCACGAGCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAAAGGTTTTCGAAG	395
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	Arabidopsis cDNA clones	Db	396	ATCGCGCTTATAAAAACCGAGATTTGCAATTAATGCGACTAATGAGACCATCAAAATGTGG	455
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	421	TTTCTTGAAGCATTTTCTTCTACACGACTAGAGATGAGCTCTTCTCAATCTCG	480
	Arabidopsis cDNA clones	Db	456	TTTCTTGAAGCATTTTCTTCTACACGACTAGAGATGAGCTCTTCTCAATCTCG	515
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	481	TTATGAGATGATACCAAGACATTTACCGGTTTGAAGCACTATATAGTTCAAAACC	540
	Arabidopsis cDNA clones	Db	516	TTATGAGATGATACCAAGACATTTACCGGTTTGAAGCACTATATAGTTCAAAACC	575
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	541	AGCGATGCTTATCTTCTATGCTCAAACTTTACACATACCAAACTTTTCAGAGGCTTGGCTT	600
	Arabidopsis cDNA clones	Db	576	AGCGATGCTTATCTTCTATGCTCAAACTTTACACATACCAAACTTTTCAGAGGCTTGGCTT	635
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	601	ATATCCATATGCTCTGGTGTCTGCGACAGAGATATATAACCAAAATCTTTTGGTTG	660
	Arabidopsis cDNA clones	Db	636	ATATCCATATGCTCTGGTGTCTGCGACAGAGATATATAACCAAAATCTTTTGGTTG	695
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	661	ATCCCAACACCATCAGTAAAGCTCTGTGATTTTGGAGTGCAGAACTACTGTTGGAAG	720
	Arabidopsis cDNA clones	Db	696	ATCCCAACACCATCAGTAAAGCTCTGTGATTTTGGAGTGCAGAACTACTGTTGGAAG	755
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	721	GTGAACCAACATATATATATCTGCTCGGTATACCGAGCTCAGAACTCATCTTTG	780
	Arabidopsis cDNA clones	Db	756	GTGAACCAACATATATATATCTGCTCGGTATACCGAGCTCAGAACTCATCTTTG	815
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	781	GTGCCACAGATATATATATATATGTTGTTGCTGCTGTTGTTGTTCTGGCAGAGC	840
	Arabidopsis cDNA clones	Db	816	GTGCCACAGATATATATATATGTTGTTGCTGCTGTTGTTGTTCTGGCAGAGC	875
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	841	TACTTCTGGCAGCGCTTATTCGGGAGAGAAATTTCTGTGACCAAGCTAGTGGAGATCA	900
	Arabidopsis cDNA clones	Db	876	TACTTCTGGCAGCGCTTATTCGGGAGAGAAATTTCTGTGACCAAGCTAGTGGAGATCA	935
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	901	TAAAGTTCTTGGTACTCCAACTCGGAAGAAATCCGGTGCATGAACCAAACTACACAG	960
	Arabidopsis cDNA clones	Db	936	TAAAGTTCTTGGTACTCCAACTCGGAAGAAATCCGGTGCATGAACCAAACTACACAG	995
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	961	ACTTCAGATTTCCCAAAATCAAAAGCCCACTTGGCATAAGGTTTTCACAAGCGGATGC	1020
	Arabidopsis cDNA clones	Db	996	ACTTCAGATTTCCCAAAATCAAAAGCCCACTTGGCATAAGGTTTTCACAAGCGGATGC	1055
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	1021	CTCGGAAGCATTTGACCTTGCACTCTGGCTTCTTCAATCTCACCAGTCTACGTTGCA	1080
	Arabidopsis cDNA clones	Db	1056	CTCGGAAGCATTTGACCTTGCACTCTGGCTTCTTCAATCTCACCAGTCTACGTTGCA	1115
TITLE JOURNAL REFERENCE AUTHORS	2 (bases 1 to 1591) Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, J.M., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.	QY	1081	CTGGCTCGAGGATGTGCGCATCGGTTTTCATGAACCTCGTGAGCAAAATGCTCGTC	1140
	Arabidopsis cDNA clones	Db	1116	CTGGCTCGAGGATGTGCGCATCGGTTTTCATGAACCTCGTGAGCAAAATGCTCGTC	1175

## ORIGIN

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 Matches 1550; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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## RESULT 3

LOCUS AY064020  
 DEFINITION Arabidopsis thaliana putative shaggy protein kinase dzeta  
 (At2g30980) mRNA, complete cds.  
 ACCESSION AY064020.1 GI:17381127  
 VERSION FLI CDNA.  
 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana

## REFERENCE

AUTHORS Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Lam, B., Satou, M., Seki, M., Shinn, P., Southwick, A., Sakurai, T., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Arabidopsis Full Length cDNA Clones  
 Unpublished

## TITLE

JOURNAL Arabidopsis Full Length cDNA Clones  
 REFERENCE 2 (bases 1 to 1566)  
 AUTHORS Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlín-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Direct Submission

## TITLE

JOURNAL Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
 COMMENT RIKEN Genomic Sciences Center  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PEGC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M.,

Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlín-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PEGC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PEGC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

## FEATURES

## source

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/db\_xref="taxon:3702"

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/note="this clone is in a modified pBluescript vector

(lambda ZAP) as a XhoI/SstI insert."

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## 3' UTR

## ORIGIN

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DEFINITION Arabidopsis thaliana (thale cress)  
ACCESSION AY087542.1 GI:21406280  
VERSION FLI CDNA.  
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SOURCE Arabidopsis thaliana  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 1503)  
AUTHORS Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,  
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.  
Full-length messenger RNA sequences greatly improve genome  
annotation  
Genome Biol. 3 (6), RESEARCH0029 (2002)  
JOURNAL MEDLINE 22088475  
PUBMED 12093376  
REFERENCE 2 (bases 1 to 1503)  
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
Feldmann,K.  
Full-length cDNA from Arabidopsis thaliana  
Unpublished  
JOURNAL 3 (bases 1 to 1503)  
REFERENCE Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
Feldmann,K.  
Direct Submission  
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
Malibu, CA 90265, USA  
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made  
available to TIGR and Genbank. The following quality assessment of  
this set was done by comparison with known proteins: two percent of  
the clones are estimated to be 5'-truncated; less than one percent  
are 3'-truncated; approximately two percent represent alternative  
splice variants, including unspliced introns and spliced exons; one  
percent may contain premature stop codons; five percent may have  
frame shifts in a coding region. A sequence is considered to be  
5'-truncated if it lacks the translation initiation start (ATG). A  
sequence is considered to be 3'-truncated if it lacks the  
C-terminal end of the encoded protein. Please note that these cDNA  
sequences are derived from the Ws or Laer ecotypes and therefore  
may contain polymorphisms when compared to sequences from Col-0.  
Genet carried out the library production and sequencing of the  
full-length clones. Ceres, Inc. carried out the clustering of the  
5' sequences, selection of clones, and sequence assembly.  
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Query Match		90.3%; Score 1478; DB 8; Length 1503;	
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QY	1381	CTGAGAAGAGATGATGTCTCTCTCTAGACGTCGCAATTCAGCTTTTTCAGAAATCAGG	1440
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QY	1441	AGCGGATGTTGTGCCCATTAATATCTTTTGTTCACCTGACTTGTAGAGAGAT	1494
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RESULT 5	AY096698	1270 bp	mRNA	linear	PLN 18-SEP-2002
LOCUS	Arabidopsis thaliana putative shaggy protein kinase dzeta				
DEFINITION	(AT2g30980) mRNA, complete cds.				
ACCESSION	AY096698				
VERSION	AY096698.1				
KEYWORDS	FLI CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
	1 (bases 1 to 1270)				
AUTHORS	Yamada, K., Ban, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayaehizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.				
	Arabidopsis Open Reading Frame (ORF) Clones				
TITLE	Unpublished				
	2 (bases 1 to 1270)				
JOURNAL	Yamada, K., Ban, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayaehizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.				
	Direct Submission				
REFERENCE	Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA				
	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN				

Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, ORFC (SSP) Consortium members constructed and sequenced the PUN1 (ORF) clones using the pAT CDNA3 Yamada K., Banh, J., Chan, M. M., Chang C. H., Chang, E., Dale, J. M., Tang J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Deng C. C., Tortum, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R., and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

**FEATURES** Location/Qualifiers

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Submitted to GenBank.  
Location/Qualifiers

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1 (bases 1 to 1572)	
Piao,H.L., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B., Kim,S.H. and	
Hwang,I.	
An Arabidopsis GSK3/shaggy-like gene that complements yeast salt	
stress-sensitive mutants is induced by NaCl and abscisic acid	
Plant Physiol. 119 (4), 1527-1534 (1999)	
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10198112	
2 (bases 1 to 1572)	
Piao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B. and	
Hwang,I.	
Direct Submission	
Submitted (18-AUG-1997) Plant Molecular Biology and Biotechnology	
Research Center, Gyeongsang National University, Chinju 660-701,	
Korea	
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RESULT 7
LOCUS AY035048 1582 bp mRNA linear PLN 18-SEP-2002
DEFINITION Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA,
complete cds.
ACCESSION AY035048
VERSION AY035048.1 GI:14334749
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabisidopsis Full Length cDNA Clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1582)
AUTHORS Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G.,
Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
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Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M.,
Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and
Theologis,A.
JOURNAL Direct Submission
COMMENT Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X.,
Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D.,
Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L.,
Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E.,
Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J.,
Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.
Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
Location/Qualifiers
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Best Local Similarity 77.5%; Pred. No. 1.8e-171;
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DEFINITION	A.thaliana mRNA for shaggy-like kinase iota.		PLN 13-FEB-1998
ACCESSION	X99696		
VERSION	X99696.1	GI:1480077	
KEYWORDS	AKS iota gene; shaggy-like kinase iota.		
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REFERENCE	1		
AUTHORS	Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.		
TITLE	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)		
JOURNAL	Plant Physiol. 113, 306-306 (1997)		
AUTHORS	2 (bases 1 to 1614)		
TITLE	Dornelas,M.C.		
JOURNAL	Direct Submission		
	Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud (Parisxi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex, FRANCE		
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# RESULT 9 AY051053

LOCUS Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA, complete cds.  
 DEFINITION

ACCESSION AY051053

VERSION AY051053.1

KEYWORDS FLI, CDNA.

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

## REFERENCE

AY051053 1255 bp mRNA linear PLN 18-SEP-2002  
 Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA, complete cds.  
 AY051053 GI:15293238  
 FLI, CDNA.  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

## AUTHORS

Yanada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Egtu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Arabidopsis Open Reading Frame (ORF) Clones  
 Unpublished  
 2 (bases 1 to 1255)  
 Yanada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

## TITLE

Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

## JOURNAL

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

## COMMENT

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yanada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,

Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Tracy, S. E., Davis, R. W., Ecker, J. R., and Theologis, A.	
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.	
Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.	
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LOCUS			
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VERSION			
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REFERENCE			
AUTHORS			
TITLE			

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JOURNAL Plant Physiol. 113, 306-306 (1997)
REFERENCE 2 (bases 1 to 1738)
AUTHORS Dornelas,M.C.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,
Institut de Biotechnologie des Plantes, Centre de Recherches sur
les Plantes, URA 1128, Biol. du Devel. des Plantes, Bat. 630, P-91405
ORSAY Cedex, FRANCE
COMMENT Corresponding genomic sequence is found in Y08947.
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SOURCE Arabidopsis thaliana (thale cress)
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AUTHORS Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.B.
TITLE Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE 22088475
PUBMED 12093376
REFERENCE 2 (bases 1 to 1636)

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AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.  
 TITLE Full-length cDNA from Arabidopsis thaliana  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 1636)  
 AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA  
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genest carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.  
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 Best Local Similarity 77.4%; Pred. No. 1.4e-126;  
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 1 (bases 1 to 1670)  
 SHINN,P., CHEN,H., CHEUK,R., KIM,C.J., MEYERS,M.C., BAHN,J., BOWSER,L., CARNINCI,P., CHANG,E., DALE,J.M., GOLDSMITH,A.D.,

Havashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Arabidopsis cDNA clones

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Unpublished

2 (bases 1 to 1670)

Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Havashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Direct Submission

Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Havashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

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## RESULT 15

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of

Agricultural Sciences Rice Full-Length cDNA Project Team;

Kikuchi, S., Satoh, K., Nagata, T., Kawagashita, N., Doi, K.,

Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,

Kojima, K., Naniki, T., Ohneda, S., Yahagi, W., Suzuki, K., Li, C.,

Ohneda, S., Shishiki, T., Foundation of Advancement of International

Science Genome Sequencing &amp; Analysis Group; Ootomo, Y., Murakami, K.,

Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,

Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,

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Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,

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Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

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Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and

Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of

Agricultural Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,

Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica

rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>

AK073725 2055 bp mRNA linear PLN 24-JUL-2003  
 Oryza sativa (japonica cultivar-group) cDNA clone:J033061120, full  
 insert sequence.

AK073725

AK073725.1 GI:32983748

FLI\_CDNA; CAP trapper.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1

The Rice Full-Length cDNA Consortium, National Institute of  
 Agricultural Sciences Rice Full-Length cDNA Project Team;

Kikuchi, S., Satoh, K., Nagata, T., Kawagashita, N., Doi, K.,

Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,

Kojima, K., Naniki, T., Ohneda, S., Yahagi, W., Suzuki, K., Li, C.,

Ohneda, S., Shishiki, T., Foundation of Advancement of International

Science Genome Sequencing &amp; Analysis Group; Ootomo, Y., Murakami, K.,

Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,

Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,

Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,

Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,

Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;

Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,

Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,

Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,

Saito, K., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,

Yoshino, M. and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

22752273

12869764

2 (bases 1 to 2055)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,  
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,  
 Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,

Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,

Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,

Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,

Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,

Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,

Namiki, T., Niikura, J., Niikura, J., Nishi, K., Nomura, K.,

Numasaki, T., Ohneda, E., Ohno, M., Ohtsuki, K., Ooka, M., Ooka, H.,

Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, K., Sakai, K.,

Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,

Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,

Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,

Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,

Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,

Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and

Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of

Agricultural Sciences, Department of Molecular Genetics, Head of

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305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,

Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica

rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>



NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ootato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

# FEATURES

source  
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/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="J033061L20"

## ORIGIN

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276 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 03:29:55 ; Search time 1283.09 Seconds  
(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: Geneseqn2000s:\*
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- 5: Geneseqn2001bs:\*
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- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
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- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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30	557	34.0	1419	3 AAC43095	Aac43095 Arabidops
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DT 18-OCT-2000 (first entry)  
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KW Hybridisation assay; Genetic mapping; Gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
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XX  
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XX  
PD 06-SEP-2000.  
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PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
PR 28-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999;	99US-0132863P.	PR 23-JUL-1999;	99US-0145145P.
PR 11-MAY-1999;	99US-0134256P.	PR 23-JUL-1999;	99US-0145218P.
PR 14-MAY-1999;	99US-0134218P.	PR 23-JUL-1999;	99US-0145224P.
PR 14-MAY-1999;	99US-0134219P.	PR 26-JUL-1999;	99US-0145276P.
PR 14-MAY-1999;	99US-0134221P.	PR 27-JUL-1999;	99US-0145913P.
PR 14-MAY-1999;	99US-0134370P.	PR 27-JUL-1999;	99US-0145918P.
PR 18-MAY-1999;	99US-0134768P.	PR 27-JUL-1999;	99US-0145919P.
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PR 21-MAY-1999;	99US-0135353P.	PR 02-AUG-1999;	99US-0146388P.
PR 24-MAY-1999;	99US-0135629P.	PR 02-AUG-1999;	99US-0146389P.
PR 25-MAY-1999;	99US-0136021P.	PR 03-AUG-1999;	99US-0147038P.
PR 27-MAY-1999;	99US-0136392P.	PR 04-AUG-1999;	99US-0147204P.
PR 28-MAY-1999;	99US-0136782P.	PR 04-AUG-1999;	99US-0147302P.
PR 01-JUN-1999;	99US-0137222P.	PR 05-AUG-1999;	99US-0147192P.
PR 03-JUN-1999;	99US-0137528P.	PR 05-AUG-1999;	99US-0147260P.
PR 04-JUN-1999;	99US-0137502P.	PR 06-AUG-1999;	99US-0147303P.
PR 07-JUN-1999;	99US-0137724P.	PR 06-AUG-1999;	99US-0147416P.
PR 08-JUN-1999;	99US-0138094P.	PR 09-AUG-1999;	99US-0147493P.
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KW protein identification; signal transduction pathway; metabolic pathway;  
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QY	129	CGTGTCCCGATATAGACACACAGAGAAATGCTGCTGCTGTTATAGAGGAAATGAT	188
DB	122	CCCGTCTCTGAATGATTTCTATAGGAAATGCTGCTGCTGTTATAGGAGAAATGAT	181
QY	189	GCTGTTACCGGTACATATTTCTACTCAATTTGGAGGCAAAATGGTGAACCTTAAACAG	248
DB	182	GCTGTTACTGTTCAATATCTTCCACTACTATAGAGGCAAAACGGGAAACCAAGCAG	241
QY	249	ACCATTTAGTTACATGGCGGAAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	308
DB	242	ACCATTTAGTTACATGGCTGAGCGGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	301
QY	309	GCAAAATGCTTGGAAATCAGTACGTTAGGCAATTTAGAGGTTTTCAGAGATCGCGT	368
DB	302	CGGAAATGCTTGGAAATCAGTACGTTAGGCAATTTAGAGGTTTTCAGAGATCGAGC	361

QY	369	TATATAAAACCGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGTTCTCTTG	428
DB	362	TATATAAAACCGAGAGTTGCAATTAATGCGACCAATGGATCACCAGATGTCTCTCTTG	421
QY	429	AAGCAATGTTCTCTCTACACAGCTAGAGATGAGTCTTCTCAATCTCGTTATGGAG	488
DB	422	AAGCACTGTTCTCTCTACACAGCTAGAGATGAGTCTTCTCAATCTCGTTATGGAG	481
QY	489	TATGTACCAGAGACATTGTACCGGGTTTTGAGCACTATACTAGTTCAAAACAGCGGATG	548
DB	482	TATGTACCTGAGACTTTATACCGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGATG	541
QY	549	CCTATCTTCTATGCTCAAACTTTACACATACCAATCTTCAGAGGCTTGCTTATATCCAT	608
DB	542	CCAATTTTCTATGCTCAAACTTTACACATACCAATCTTTAGAGGTTTGGCTTACATCCAT	601
QY	609	ACTGCTCTGCTGCTGCTGCGACAGATATAAACAACACAAAATCTTTTGGTTGATCCCCAC	668
DB	602	ACTGTTCCCGGTTTGGCAGAGATGTGAACAACACAAAATCTCTTGGTTGATCCCTTG	661
QY	669	ACCCATCAGTGTAACTCTGTGATTTTGAAGTCAAAAGTACTGGTGAAGGTGAACCA	728
DB	662	ACCCATCAGTGTAACTCTGTGATTTTGAAGTCAAAAGTACTGGTGAAGGTGAACCA	721
QY	729	AACATATCATATATCTGCTCTCGGTATTACGAGCTCCAGAACTCATCTTTGGTGCACA	788
DB	722	AACATATCATATATCTGCTCTCGGTATTATCGTGTCTCAGAACTCATCTTTGGCACA	781
QY	789	GAGTATACATCATCTGATGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	848
DB	782	GAGTATACATCATCTGATGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	841
QY	849	GGCAGCGCTTATTTCCCGGAGAAAATTTCTGGGACCACTAGTGGAGATCATAAGGTT	908
DB	842	GGCAGCGCTTATTTCCAGGAGAAAATTTCACTGATCAGCTTGTGGAGATCATAAGGTT	901
QY	909	CTTGTGATCTCAACTCGCGAGAGAAAATCGGTCATGAAACCCAAATACACAGATTCAG	968
DB	902	CTTGTGATCTCAACTCGTGAAGAAAATCGATATGAACCCGAACTACACAGATTTAGG	961
QY	969	TTCCCAAAATCMAAGCCCACTTGGCATAGGTTTTCCCAAGGGATGCTCCGGA	1028
DB	962	TTCCCAAAATCMAAGCTCACTTGGCATAGGTTTTCCCAAGGGATGCTCCGGA	1021
QY	1029	GCCATTGACCTTGATCTCGGCTTCTCAATCTCAAGTCTAGTGGAGTCTGCTGCTGCTG	1088
DB	1022	GCAATAGACCTTGATCTCGGCTTCTCAATCTCAAGTCTAGTGGAGTCTGCTGCTGCTG	1081
QY	1089	GAGCATGTGCGCATCTCGTTTTTCAATGAACTCCGTGAGCCAAATGCTGCTTCCAAAT	1148
DB	1082	GAGCATGTGCTCATCTCGTTTTTCAATGAACTCCGTGAGCCAAATGCTGCTTCCAAAT	1141
QY	1149	GGCCGACCTTACCACTGCTGCTTCAACTTCAAGAGAGTTGCTGCTGCTGCTGCTGCTG	1208
DB	1142	GCTGCTCATTTACCGCCATTTTCAATTTCAAAAGAGTTAGTGGAGTCTCAATTTGAG	1201
QY	1209	CTTATCAACAGCTTAATACAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTTCAAT	1268
DB	1202	CTAATCAACAGCTTAATACAGAGCATGTGAGGCGACAGATGAATGGAGGATTTACAA	1258
QY	1269	CAAGCTGGACCTTGAAGAGCATCTCGAGATGCTTTTCCAGAGCAAAATGCGGCTTAT	1328
DB	1259	AACAGTTAAAGAACTGTGATGTCTGAGAGAAAGAGGAGAAAGCGGTTTACTACTTTT	1318
QY	1329	GGAATGAAGGAGAGGAGATTTACTTCTCTGATTAATCAAGTATCAGTCTTCTGAGAG	1388
DB	1319	ATTGATAGTTGACAGGTTTCAACAGTATCTTAAACCAAGCTATTTATCAGCTTTATAC	1376
QY	1389	AGATGATGCTCTCTCTTTAGAGCTGGCAATTTCACTTTTGGAGAAATCAGGAGCGGAT	1448
DB	1377	-----CCGTAGTAAAGTCATATTTCACTTTTGGAGAAATCAGATGCTGATA	1422





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Db      1228 CTGATCATAGGCTCTCCAGAGCATATAGCGCGCAGATGGTCTCAGCTTCGGCAT 1287
QY      1269 CAAGCTGGACCTAGA 1284
Db      1288 TCTGCCGGTACATAGA 1303

RESULT 5
AAC47997
ID AAC47997 standard; DNA; 1657 BP.
XX
AC AAC47997;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 16-APR-1999; 99US-0129845P.
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PR 21-APR-1999; 99US-0130449P.
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PR 28-APR-1999; 99US-0131449P.
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PR 07-MAY-1999; 99US-0132487P.
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PR 14-MAY-1999; 99US-0134218P.
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PR 14-MAY-1999; 99US-0134221P.
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PR 19-MAY-1999; 99US-0134941P.
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PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 28-JUN-1999; 99US-0140823P.
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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 27-JUL-1999; 99US-0145913P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.

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PR	12-AUG-1999;	99US-0148341P.	QY	197	CGGTACACATAATTTCTACTACAAATTTGGAGGCAAAATGCTGAACCTTAACACAGACCAATTAG	256
PR	13-AUG-1999;	99US-0148565P.	Db	136	TTGTATATATTTCCACACAAATCGGTGGCAAAATGCTGAACCAAAACAGACCAATTAG	195
PR	16-AUG-1999;	99US-0149368P.	QY	257	TTACATGGCCGAACGTGTTGGAAACAGGATCAATTCGGAATTTGATTTCCAGGCAAAATG	316
PR	17-AUG-1999;	99US-0149175P.	Db	196	TTACATGGCCGAGCGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTCCAAAGCAAAATG	255
PR	20-AUG-1999;	99US-0149722P.	QY	317	CTTGGAACTCGGAAATCAGTAGCCATTAAGAAGGTTTGGCAAGATCGCGGTTTATAAAAA	376
PR	20-AUG-1999;	99US-0149723P.	Db	256	TTTGGAGACTGGAGAAACCGTGGCAATAAAGAGGTTTGGCAAGATGAAGATACAAAGAA	315
PR	23-AUG-1999;	99US-0149902P.	QY	377	CCGAGAGTTGCAATTAATGCGACTAATGACCAATCCAAATGTGGTTTCTTGAAGCAATTG	436
PR	25-AUG-1999;	99US-0150566P.	Db	316	CCGAGAACTTCAGTTGATCGGTGATGATCATCCGAATGTGGTTTGTGTAAGCATTTG	375
PR	26-AUG-1999;	99US-0150884P.	QY	437	TTTCTTCTCAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTTATGGAGTATGTACC	496
PR	27-AUG-1999;	99US-0151065P.	Db	376	CTTCTTTTTCGACTCAAGTAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCCC	435
PR	27-AUG-1999;	99US-0151066P.	QY	497	AGAGACATTTGACCGGTTTTCGAAGCACTATCTAGTTCAAACCCAGCGATGCTATCTT	556
PR	30-AUG-1999;	99US-0151303P.	Db	436	TGAGAGCTTGTATCGAGTTCTGAAACATTTATAGTAGTGAACCAAGAAATGCTCTTGT	495
PR	31-AUG-1999;	99US-0151304P.	QY	557	CTATGTCAAATTTTACACATACCAATCTTCAGAGGCTTGGCTTATATCATCTACTCTCC	616
PR	01-SEP-1999;	99US-0151309P.	Db	496	CTATGTTAACTTTACATGATATCAGATCTTCGGGACCTTGTCTACATTCACAATGTGC	555
PR	07-SEP-1999;	99US-0152363P.	QY	617	TGGTGTCTGCCACAGAGATATAAACCAAAATCTTTTGGTTGATCCCAACACCCATCA	676
PR	10-SEP-1999;	99US-0153070P.	Db	556	TGGAGTTTGTCAAGAGATCTAAAGCCTCAAATCTTCTGGTTGATCTCTTACTCATCA	615
PR	13-SEP-1999;	99US-0153758P.	QY	677	GTGTAAGCTCTGTGATTTTGGAAAGTGCAAAAGTACTGTGTGAAGGTGAACCAACATATC	736
PR	15-SEP-1999;	99US-0154018P.	Db	616	AGTCAAAATCTGTGACTTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAAGCAACATTC	675
PR	16-SEP-1999;	99US-0154039P.	QY	737	ATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTTGGTGCACAGAGTATAC	796
PR	20-SEP-1999;	99US-0154779P.	Db	676	TTACATCTGCTCACGANTCTACCGTGCAACCCGAGCTCATATTTGGTGCACCTGAGTACAC	735
PR	22-SEP-1999;	99US-0155139P.	QY	797	ATCATCCATGATATATGCTGCTGGTTGTTGTTCTGGCAGAGACTACTTCTTGGGAGCC	856
PR	23-SEP-1999;	99US-0155486P.	Db	736	AACCTTCTATTTGATATCTGCTGCTGTTGTTGTTCTTGTGAGCTTCTTCTTGGTCAACC	795
PR	24-SEP-1999;	99US-0155659P.	QY	857	GTATTTCCCGGAGAAATTTCTGTGACCAAGCTAGTGGAGATCATAAAGTTCTTCTGGTAC	916
PR	28-SEP-1999;	99US-0156458P.	Db	796	ATTATTTCCCGGAGAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAGTTCTTGGTAC	855
PR	29-SEP-1999;	99US-0156596P.	QY	917	TCCAACCTCGGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCAACA	976
PR	04-OCT-1999;	99US-0157117P.	Db	856	ACCAACTCGGAAGAAATTCGTTGTATGAATCCACATTCACACAGATTCAGGTTTCCACA	915
PR	06-OCT-1999;	99US-0157753P.	QY	977	AATCAAAGCCACCTTTGGCATAAAGTTTTCACAAGCGGATGCTTCCGGAAGCCATTGA	1036
PR	08-OCT-1999;	99US-0158023P.	Db	916	GATAAAGGCACATCCGTGGCACAAGATCTTCCAACAAAGGATGCCCCGGAAGCGATTGA	975
PR	12-OCT-1999;	99US-0158369P.	QY	1037	CCTTGCATCTCGGCTTCTTCAATACTCACCAAGTCTACGTTGACCTGCGCTCGAGGCATG	1096
PR	13-OCT-1999;	99US-0159293P.	Db	976	TTTTTGATCAAGGCTCTTCAATACTCTCAAGTCTAAGATGACAGAGCGCTCGAAGCTTG	1035
PR	13-OCT-1999;	99US-0159294P.	QY	1097	TGCGCATCCGTTTTTCAATGAATCCGTTGAGCGCAAAATGCTCGTCTTCCAAATGCCGACC	1156
PR	14-OCT-1999;	99US-0159330P.	Db	1036	TGCACATCCGTTCTTTGATGAACTCAGAGAGCCAAACGCTCGTTTACCAAATGGAGACC	1095
PR	14-OCT-1999;	99US-0159331P.	QY	1157	TTTACCAACCGTTTCAACTTCAACCAAGAGTTGCTGGGGCTTACCGGAGCTTATCAA	1216
PR	18-OCT-1999;	99US-0159637P.	Db	1096	TTTCCGCGCTCTTTTCAACTTCAACCAAGAGAGTGTGGATCATCATCCTCACTGAGTCAA	1155
PR	21-OCT-1999;	99US-0160814P.	QY	1217	CAGGCTAAATACAGACGATGTGAGGCGACAGATGAATGGTGGCTTTTCCATTTCAAGCTGG	1276
PR	21-OCT-1999;	99US-0160815P.	Db	1156	CAAGTTGATTCACAGACCATATCAAGAGACAAATTTGGGTCTAAGCTTCTTGAATCAATCTGG	1215
PR	21-OCT-1999;	99US-0160815P.	QY	1277	ACCTAGAAAAAG	1288

Query Match 45.0%; Score 736; DB 3; Length 1657;  
 Best Local Similarity 77.4%; Pred. No. 3.6e-102;  
 Matches 892; Conservative 0; Mismatches 260; Indels 0; Gaps 0;  
 137 CGATATAGACAACGACAGAAATGCTGCTGTTATAGAGAAATGATGCTGTTAC 196  
 76 CGCATGGCTGATGAAGAGATGCTGCTGTTAGTTGAGGACATGATCAAGTAC 135

Db 1216 AACTTAAAGG 1227

RESULT 6  
AAL54221  
ID AAL54221 standard; cDNA; 1490 BP.  
XX AAL54221;  
AC AAL54221;  
XX 27-MAR-2003 (first entry)  
XX cDNA of wild-type DWf12 protein.  
DB DWf12; transgenic plant; plant breeding; industrial application;  
KW agricultural production; gene; ss.  
XX Unidentified.  
OS  
FH Key Location/Qualifiers  
FT CDS 200..1312  
FT /\*tag= a  
FT /product= "Protein of wild-type DWf12 locus"  
XX  
PN WO200292777-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 15-MAY-2002; 2002WO-US015563.  
XX  
PR 16-MAY-2001; 2001US-0291342P.  
XX  
PA (ARIZ-) ARIZONA BOARD OF REGENTS.  
XX  
PI Choe S, Feldmann K, Tax F;  
XX  
DR WPI: 2003-129285/12.  
DR P-PSDB; AAO26726, AAO26727.  
XX  
XX New isolated DWf12 mutant polypeptide for producing transgenic plants  
PT displaying altered biochemistry, structure or morphology which are useful  
PT in plant breeding, in agricultural production or industrial applications.  
XX  
XX Example 2; Fig 2; 62pp; English.  
XX  
CC The invention relates to an isolated DWf12 (DWf12) mutant polypeptide.  
CC The mutant polypeptide comprises at least 70 % sequence identity to the  
CC amino acid sequence of the DWf12 polypeptide given in the specification  
CC at positions 38-326 or 1-380, and having a mutation of at least one non-  
CC conservative substitution, addition or deletion of an amino acid in a  
CC region of the polypeptide corresponding to a region given in the  
CC specification. The mutant DWf12 polypeptide is useful in producing  
CC transgenic plants that display at least one altered DWf12 phenotype, such  
CC as altered biochemistry, structure or morphology. The transgenic plant  
CC can be used in plant breeding or directly in agricultural production or  
CC industrial applications. The polynucleotide is useful in isolating or  
CC creating other mutant cell gene alleles, in inhibiting or enhancing  
CC endogenous DWf12 gene expression, and in standard diagnostic assays as  
CC hybridization probe or primer. This polynucleotide sequence represents  
CC the cDNA of the wild-type DWf12 locus of the invention  
XX  
SQ Sequence 1490 BP; 413 A; 340 C; 297 G; 440 T; 0 U; 0 Other;  
Query Match 44.8%; Score 733; DB 10; Length 1490;  
Best Local Similarity 77.4%; Pred. No. 1e-101;  
Matches 889; Conservative 0; Mismatches 260; Indels 0; Gaps 0;  
XX 137 CGATATAGACACGACGAAATGCTGCTCTGTATAGAGGAAATGATGCTGTAC 196  
DB 196 CGCCATGGCTGATGATAGGAGATGCTGCTGTGTGTGATGACATGATCAAGTCAC 255  
XX 197 CGGTACATATTTCTACTAGATTTGGAGGCAAAATGCTGAACCTTAACAGACATTAG 256

Db 256 TGGTCATATTATTTCCACCACCAATCGGTGGCAAAATGCTGAACCAACACGACAAATTAG 315  
QY 257 TTACATGCCGAAACGTGTGTTGGAAACAGAGATCATTCGGAATATGTTATTCAGGCAAAATG 316  
Db 316 TTACATGCCGAGCGAGTGTGTTGGTACAGGCTCGTTCGGGATCGTTCCTCAAGCAAAATG 375  
QY 317 CTTCGAAACTCGGAATCAGTAGCCATTAAGAGGTTTTCGAAGATCCCGCTTATAAATA 376  
Db 376 TTTGGAGACTGGAGAAACCGTGGCGATTAAGAGGTTTTCGAAGATAGAGATACAAGAA 435  
QY 377 CCGAGAGTTGCAATTAATGCGACTTAATGAGACCATCAAAATGTGGTTTCTTGAAGCAATTG 436  
Db 436 CCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGTGGTTTTCGAAGCAATTG 495  
QY 437 TTTCTTCTCAACGACTAGAGATGAGCTTCTCAATCTCGTATGATGAGATGATGATCC 496  
Db 496 CTTCTTTTCGACTACAAGTAAAGACGAGCTTTCTTGAACCTTGGTTATGGAGTATGTC 555  
QY 497 AGAGACATTGTACCGGTTTTCGAGCACTATATAGTTTCAACACGAGCGATCCCTATCTT 556  
Db 556 TGAGAGCTTGTATCGAGTTCTGAACCATTAATAGTAGTGAACCAAGAAATGCTCTTGT 615  
QY 557 CTATGTCAAACTTTACACATACCAAACTCTCAGAGGCTTGGCTTATATCCATCTACTGCTCC 616  
Db 616 CTATGTAAACTTTACATGATCAGATCTTCGGGACTTGTCTACATTCACATGTTGC 675  
QY 617 TGGTGTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACACCATCA 676  
Db 676 TGGAGTTTGTACAGAGATCTAAAGCCTCAAACTCTTCTGGTTGATCTCTTACTCATCA 735  
QY 677 GTGTAAGCTCTGTGATTTTGAAGTGAAGAGTACTGCTGAAGGTGAACCAACATATC 736  
Db 736 AGTCAAAATCTGTGACTTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAAGCAACATTC 795  
QY 737 ATATATCTGCTCTCGTATTATCCGAGCTCCAGAACTCATCTTTGGTGCACAGAGTATAC 796  
Db 796 TTACATCTGCTCAGATTTCTACCGTGACCCGAGCTCATATTTGGTGCACACTGAGTACAC 855  
QY 797 ATCATTCATGATATATAGTCTGTGTTGTGTTCTGCGAGAGTACTTCTTGGGAGCC 856  
Db 856 AACTTCTATTGATATCTGCTGTGTTGTGTTCTTCTGCTGAGCTTCTTCTTGGTCAGCC 915  
QY 857 GTTATTCGGGAGAAATTTCTGTGGACAGCTAGTGGAGATCATAAAGTTCTTGGTAC 916  
Db 916 ATTAATTTCCCGGAGAAATGCTGTGGATCAGCTCGTTGAAATTAATAAAGTTCTTGGTAC 975  
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Db 976 ACCAACTCGAGAGAAATCCGTTGTATGATCCATTTACAGATTTTCAAGTTTCCCA 1035  
QY 977 AATCAAGCCACCCCTTGGCATAAGTTTTCACAAAGCGGATGCTCCGGAAGCCATTGA 1036  
Db 1036 GATAAAGGCACATCCCTGGCAAGATCTTCCACAAAGAGTGCCTCCCAAGAGCGATTGA 1095  
QY 1037 CTTGTCATCTGGCTTCTTCAATCTACCAAGTCTAGTTGCTGCTGCTGCTGCGGCATG 1096  
Db 1096 TTTTGCATCAAGGCTGCTTCAATCTCTCCAAGTCAAGATGACACAGCGCTCGAAGCTTG 1155  
QY 1097 TGCGCATCCGTTTTCATGAATCTCCGTGAGCAAAATGCTGCTTTCAAATGGCGGACC 1156  
Db 1156 TGCATATCCGTTCTTTGATGAATCTCAGAGAACCAACCGTCTGTTTACCAATGGAGCGCC 1215  
QY 1157 TCTACCACTGTTTCAACTTTCAAAACAGAGTTGTCTGGGGCTTCCCGGAGCTTATCAA 1216  
Db 1216 TTTCCGCGCTCTCTTCAACTTTCAAAACAGAGTGTGATCATCACCTGAACTGGTCAA 1275  
QY 1217 CAGGCTAATACAGAGCATGTGCGGCGACAGATGATGCTGCTTTCATTTCAAGCTGG 1276  
Db 1276 CAAGTTGATTTCCAGACCATCAAGAGACAAATGGGCTCTAAGCTTCTTGAATCAATCTGG 1335  
QY 1277 ACCCTAGAA 1285  
Db 1336 AACTTAAAA 1344

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RESULT 7
AAC47206
ID AAC47206 standard; DNA; 1745 BP.
XX AC AAC47206;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52951.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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AC	ABZ13070;	Db	301	TTTTCGACTACAAGTAAAGACGAGCTTTTCTTGAACCTGGTTATGAGATATGTCCTGAG	360
XX					
DT	21-JAN-2003 (first entry)	QY	501	ACATTGTACCGGGTTTGAAGCACTATAGTTTAAACAGCGGATGCTATCTTCTAT	560
XX					
DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 875.	Db	361	AGCTTGTATCGAGTTCTGAAACATTATAGTAGTCAAAACCAAGAATGCTCTTGTCTAT	420
XX					
KW	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	QY	561	GTCAAACTTTACACATACCBAATCTTCAGAGGCTTGGCTTATATCCATCTGCTCCTGT	620
XX					
OS	Arabidopsis thaliana.	Db	421	GTAAACCTTACATGATCAGATCTTCGGGACCTTGTACATTCACAATGTTGCTGA	480
XX					
PN	WO200216655-A2.	QY	621	GTCTGCCACAGAGATATAAAACCAAAAATCTTTTGGTTGATCCCCACACCCATCATGT	680
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PD	28-FEB-2002.	Db	481	GTTCGTCACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTTACTCATCAAGTC	540
XX					
PF	24-AUG-2001; 2001WO-US026685.	QY	681	AAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGGTGAAGAGGTGAACCAACATATCATAT	740
XX					
PR	24-AUG-2000; 2000US-0227866P.	Db	541	AAAACTCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAAGCCCAACATTTCTTAC	600
PR	26-JAN-2001; 2001US-0264647P.				
PR	22-JUN-2001; 2001US-0300111P.	QY	741	ATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATACATCA	800
XX					
PA	(SCRI ) SCRIPPS RES INST.	Db	601	ATCTGCTCACGATCTTACCGTGACCCGAGCTCATATTTGGTGCCACTGAGTACACACT	660
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.				
XX	Harper JF, Kreps J, Wang X, Zhu T;	QY	801	TCCATTGATATATGCTGCTGTTGTGTTCTGGCAGAGTACTTCTTGGGAGCCGCTTA	860
XX					
PI	WPI; 2002-304127/34.	Db	661	TCTATTGATATCTGGTCTGCTGTTGTTCTTCTGCTGAGCTTCTTCTTGGTCAGCCATTA	720
XX					
DR	Identifying a stress condition to which a plant cell has been exposed and	QY	861	TTCCCGGGAGAAAATCTGTGACACGCTAGTGGAGATCATAAAGTTCTTGGTACTCCA	920
XX	producing plants with increased tolerance to these abiotic stresses.	Db	721	TTTCCCGGAGAAAATGCTGTGGATCAGCTCGTTGAAATTAATAAAGTTCTTGGTACACCA	780
XX					
PS	Claim 144; SEQ ID NO 875; 577bp + Sequence Listing; English.	QY	921	ACTCCGGAAGAAATCCGGTGCTGATGAACCCAAACTACACAGACTTCAGATTCCCACAAAATC	980
XX					
CC	The invention relates to identifying a stress condition to which a plant	Db	781	ACTCGAGAAGAAATCCGTTGTATGAATCCACATTCACAGATTCAGGTTTCCACAGATA	840
CC	cell has been exposed, comprising: (a) contacting nucleic acid				
CC	representative of expressed polynucleotides in the plant cell with an	QY	981	AAAGCCCACTTGGCATAAAGTTTTCACAAGCGGATGCTCCGGAAGCCATTGACCTT	1040
CC	array or probes representative of the plant cell genome; and (b)	Db	841	AAGGCACATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCCAAGCGATTGATTTT	900
CC	detecting a profile of expressed polynucleotides in the plant cell				
CC	characteristic of a stress response. The method is useful in the	QY	1041	GCATCTGGCTCTTCAATACTCACCAAGTCTACGTTGACCTGCGCTCGAGGATGTGCG	1100
CC	production of transgenic plants, cells and seeds and in producing plants	Db	901	GCATCAAGCTGCTTCAATACTCTCAAGCTTAAGATGCACAGCGCTCGAAGCTTGTGCA	960
CC	with increased tolerance to abiotic stress. The present sequence is that				
CC	of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used	QY	1101	CATCCGTTTTTCAATGAACTCCGCTGAGCCAAATGCTCGTCTTCCAAATGGCCGACCTCTA	1160
CC	in methods of the invention. Note: The sequence data for this patent is	Db	961	CATCCGTTCTTTGATGAATTCAGAGAACCAAGCTCGTTTACCAATGGACGCGCTTC	1020
CC	not represented in the printed specification but is based on sequence				
CC	information supplied to Derwent by the European Patent Office	QY	1161	CCACCGTTTTCAACTTCAAAACAAGAGTTGTCTGGGGCTTCCACCGAGCTTATCAACAGG	1220
XX					
SQ	Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;	Db	1021	CCGCTCTCTTCAACTTCAAAACAAGAGTAGCTGGATCATCACTGAACTGGTCAACAAG	1080
	Query Match 44.7%; Score 730.8; DB 6; Length 1143;				
	Best Local Similarity 77.5%; Pred. No. 2.2e-101;	QY	1221	CTAATACACAGAGATGTGAGGCGACAGATGAATGGTGGCTTCCATTTCAAGCTGGACCC	1280
	Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;	Db	1081	TTGATTTCCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGAACT	1140
QY	141 ATAGACAACGACGAAGAAATGTCTGCTGTTTATAGAAGAAATGATGCTGTACCGGT	QY	1281	TA 1282	
Db	1 ATGGCTGATGATAAGGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGT	Db	1141	TA 1142	
QY	201 CACATATTTCTACTACAAATGGAGCAAAAATGGTGAACCTTAAACAGACCATAGTTAC				
Db	61 CATATATTTTCCACCAATTCGGTGGCAAAAATGGTGAACCAAAAACAGACAATTAGTTAC				
QY	261 ATGGCCGAACGTGTTGTTGAACAGGATCATCTCGGAATCTGTTTCCAGGCAAAATGCTTG				
Db	121 ATGGCGGAGCGAGTTGTTGTACAGGCTCGTTCCGGATCGTTTCCNAGCAAAATGTTTG				
QY	321 GAAACTGGAGAAATCAGTAGCCATTAAAGAGTTTTCAGAGATCGCCGTTATAAAAAACCGA				
Db	181 GAGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCAGAGATAGAAGATACAAGAACCGA				
QY	381 GAGTTGCAATTAATGCGACTAATGGACCATCCAAATGCGTTTCCCTTGAGCAATGTTTC				
Db	241 GAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTTGTTTGAAGCAATGCTTC				

RESULT 9  
ADN73384  
ID ADN73384 standard; cDNA; 1143 BP.  
XX ADN73384;  
XX AC  
XX AC  
DT 15-JUL-2004 (first entry)  
XX Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1279.  
DE gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;  
KW growth regulator; animal feed product; thale cress;

cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

Arabidopsis thaliana.

WO2004035798-A2.

29-APR-2004.

20-OCT-2003; 2003WO-BF011658.

18-OCT-2002; 2002EP-00079408.

(CROP-) CROPDESIGN NV.

Inze D, De Veylder L, Vlieghe K;

WPI; 2004-348466/32.

P-PSDB; ADN73385.

Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprising modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

Claim 1; SEQ ID NO 1279; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up- or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polynucleotide sequence is the cress cDNA upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa transcription factor, given in an exemplification of the invention.

Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;

Query Match 44.7%; Score 730.8; DB 12; Length 1143;

Best Local Similarity 77.5%; Pred. NO. 2.2e-101;

Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

141 ATAGACAACGACGAAATGCTGCTGCTGTATAGAGGAATGATCTCTTACCGT 200

1 ATGGCTGATGAAGAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGGT 60

201 CACATAATTTCTACTACAAATGGAGCAAAAATGGTGAACCTTAAACAGACCATTAAGTTAC 260

61 CATATATTTCCACCACATCGGTGGCAAAATGGTGAACCAACAGACCATTAAGTTAC 120

261 ATGGCGGAACGTTGTTGGAGACAGATCATTCGGAAATGTATTCAGGCAAAATGCTTG 320

121 ATGGCGGAGCGAGTTGTTGGTACAGCTCGTTCCGGATCGTTTCCAGCAAAATGTTTG 180

321 GAACTGGAGATCAGTACGATTAAGAGGTTTTCAGAGTCGCGTTATTAACCAACCA 380

181 GAGACTGGAGAACCGTGGCGATAAAGAGGTTTTCAGAGTAGAGATACAGAACCA 240

381 GAGTTCGAATTAATGCACTTAATGGACCATCAAAATGTTTCTTGAAGCATTTGTTTC 440

241 GAACCTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 300

441 TTCTCTACACGACTAGAGATGAGTCTCTTCTCAATCTCTGTTATGGAGTATGTACACGAG 500

301	TTTTGCAGTACAAAGTAAAGACGAGCTTTCTTGAACCTTGGTATGAGTATGTCCCTGAG	360
501	ACATTGTACCGGTTTTGAAGCACTATAGTTCATAACACGAGGATGCTTCTCTAT	560
361	AGTTGTATCGAGTTCTGAAACATTAATAGTAGTGCACCAACCAAGATGCTTCTCTAT	420
561	GTCAAACTTTACATACATAACAAATCTTCAGAGGCTTGGCTTATATATCATCTGCTCTGT	620
421	GTAAACCTTTACATATCATGATCTTCGGGACCTGCTTACATTCACAAATGTTGCTGA	480
621	GTCTGCCACAGAGATATAAACAACCAAAATCTTTGGTGTATGCCACACCCATCAGTGT	680
481	GTTCGTACAGAGATCTAAAGCCTCAAAATCTTCGGTGTATGCTTCTTACTCATCAAGTC	540
681	AAAGCTCTGTGATTTTGGAAAGTCTAAAGTCTGTTGAAAGGTGAACCAACATATCATAT	740
541	AAATCTGTGACTTTGGCAGTCTGGAACAGCTCGTTAAAGGTGAAGCCACATTTCTTAC	600
741	ATCTGCTCTCGTATTAACGAGCTCCAGAACTCATCTTTGGTGGCCACAGATATACATCA	800
601	ATCTGCTCAGGATCTACCGTGCACCCGAGCTCATATTTGGTGGCCACTGAGTACACAACT	660
801	TCCATTGATATATGCTCTGCTGCTGTTGTTCTGGCAGAGCTACTTCTTGGGAGCGGTTA	860
661	TCATTTGATATCTGCTGCTGCTGTTGTTCTTGTGAGCTTCTTCTTGGTCAAGCATTA	720
861	TTCCCGGAGAAATTTCTGTGACAGCTAGTGGAGATCATAAAGCTTCTTGGTACTCCA	920
721	TTTCCCGAGAAATTTCTGTGATCAGCTGCTGTTGAAATTAATAAAGTCTTGGTACCA	780
921	ACTCGGAAGAAATCCGTTGCAATGAACCAACTACACAGACTTCAGATTTCCCAAAATC	980
781	ACTCGGAAGAAATCCGTTGATGAATCCATTAACACAGATTTTCAGGTTTCCACAGATA	840
981	AAAGCCCACTTGGCATAAGTTTTCACAGCGGATGCTTCCGGAAGCCATTGACCTT	1040
841	AAAGCAGATCTCCCTGGCAAGATCTTCCACAAAGGATGCTCCCAAGGCGATTGATTTT	900
1041	GCATCTCGGCTTCTTCAATCTACCAAGTCTACGTTGACCTGCGCTCGAGGATGTGGG	1100
901	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCAAGCGCTCGAAGCTGTGCA	960
1101	CATCGGTTTTCAATGAATCCGTCAGGCAAAATGCTGCTTTCCAAATGGCCGACTCTTA	1160
961	CATCGGTTTTGATGAATCAGAGAACCAACGCTCGTTTACCAAAATGCGCGCTTTC	1020
1161	CCACGTTGTTCAACTTCAACAGAGTTGCTTGGGCTTTCACCGGAGCTTATCAACAG	1220
1021	CGGCTCTCTTCAACTTCAACAGAGTAGTGGATCATCACTGAACTGGTCAACAG	1080
1221	CTAATACAGAGATGTGAGGCGACAGATGAATGTTGGCTTTCCATTTTCAAGCTGGACC	1280
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1141	TA 1142	

RESULT 10

AAC41916

ID AAC41916 standard; DNA; 1635 BP.

XX AAC41916;

AC AAC41916;

XX 17-OCT-2000 (first entry)

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 33613.

DE Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

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PR	21-JUN-1999;	PR	27-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	PR	07-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	PR	10-SEP-1999;	99US-0153070P.





CDS 132..1277  
 /\*tag= a  
 /product= "BnPK-2"  
 WO2003040171-A2.  
 15-MAY-2003.  
 12-NOV-2002; 2002WO-US036374.  
 09-NOV-2001; 2001US-0346096P.  
 (BADI ) BASF PLANT SCI GMBH.  
 Van Thielon N, Da Costa E SilvaO, Chen R;  
 WPI; 2003-441522/41.  
 P-PSDB; ABR42363.  
 New protein kinase stress-related polypeptide coding nucleic acid, useful  
 for producing transgenic plants with an increased tolerance to an  
 environmental stress, e.g. high salinity, as compared to a wild type  
 variety of the plant.  
 Claim 1; Page 90-91; 11pp; English.  
 The present sequence is a full-length cDNA encoding BnPK-2, a novel  
 canola protein kinase stress-related polypeptide (PKSRP). The cDNA was  
 identified on the basis of homology to Physcomitrella patens PK-3 (see  
 ACC57962) and PK-10 (see ACC57966) sequence. BnPK-2 is an example of  
 PKSRPs of the invention that are important for modulating a plant's  
 response to environmental stress. Over-expression of PKSRP coding nucleic  
 acids in a plant results in the plant's increased tolerance to  
 environmental stress. Transgenic monocot and dicot plants are provided  
 that show increased tolerance to high salinity, drought and low  
 temperature  
 Sequence 1621 BP; 450 A; 371 C; 331 G; 469 T; 0 U; 0 Other;  
 Query Match 43.3%; Score 709; DB 8; Length 1621;  
 Best Local Similarity 76.6%; Pred. No. 4.2e-98;  
 Matches 868; Conservative 0; Mismatches 265; Indels 0; Gaps 0;  
 QY 161 GTCTGCTGCTTATAGAGGAATATGCTGTTCACGGTCACATAATTTCTACTACAAT 220  
 DB 155 GCCGGCTGCTGTAGTGTGACATGACCAAGTCATCTGCCACATAATCTCCACCAAT 214  
 QY 221 TGGAGGCAAAATGGTGAACCTAAACAGACCATTAGTTACATGCCGCAACGTTGTGG 280  
 DB 215 CGGTGGTAAACCGAGAACCAAAACAGACAATAAGTTACATGGCGGAGCGAGTTGTGG 274  
 QY 281 AACAGGATCATTCGGAAATTGTATTCAGGCAAAATGCTTGGAACTGGAGAAATCAGTAGC 340  
 DB 275 TACAGGCTCCTTCGGGATAGTGTTCAGGCGAAATGCTTGGAGACTGGAGAAACCGTGGC 334  
 QY 341 CATTAGAAGGTTTTCGAAGTCCCGTTATAAAACCGAGAGTTCGAATTAATGGGACT 400  
 DB 335 GATAAGAAGGTTTTCGACACAGGAGGTACAAGACCGAGAGCTTCAGCTGATGGTGT 394  
 QY 401 AATGGACCATCCAAATGTGTTTCTTTGAAGCAATTTGTTCTTCTACACGACTAGAGA 460  
 DB 395 GATGGACCATCCGAATGTTGTTTGTGAGCATGCTCTCTCTCGACACGAGCAAGA 454  
 QY 461 TGAGCTCTCCTCAATCTGTTATGAGTATGATACCGAGACATTTGACCGGTTTGAA 520  
 DB 455 CGAGCTGTTTCTGAACCTTGGTATGAGTATGTCCTCGAGAGCTTGTACCGAGTTCTGAA 514  
 QY 521 GCCTTACTAGTTCAAACACGCGGATCGCTATCTTCTATGTCAAACTTTACACATACCA 580  
 DB 515 ACATTACGACCTGCTTACACGAGGATCGCGCTGTTTATGTTAACTCTATATGATACCA 574  
 QY 581 AATCTTTACAGGCTTGGCTTATATCCATCTGCTCCTGGTGTCTGCCACAGAGATATAA 640

DB 575 GATCTTCAGAGGACTTGTCTTACATTCACAATGTTGCTGGAGTTTGTCCAGAGATCTAAA 634  
 QY 641 ACCAAGAAATCTTTTGGTTGATCCCAACACCATCAGTCTAGTCTGATTTTGGAG 700  
 DB 635 GCCTCAAAATCTTCTGGTTGATCCTCTGACTCATCAAGTGAAGATCTGTAATTTGGCAG 694  
 QY 701 TGCAAAAGTACTGTGTAAGGTGAACCAACATATCATATATCTCTCGGTATTACCG 760  
 DB 695 TCGGAACAGCTTGTTAAGGTGAAGCAACATCTTACATATGTTCAAGATTTCTACCG 754  
 QY 761 AGCTCCAGAACTCATCTTTGGTGCCACAGATATACATCATCATTTGATATATGTTCTGC 820  
 DB 755 TGCACCTGAATTAATTCGGTGCCACTCAGTACACAACTTCATTTGATATTTGGTCTGC 814  
 QY 821 TGGTTGTGTTCTGGCAGAGCTACTTCTTGGGAGCGGTTATTTCCCGGGAGAAATTTCTGT 880  
 DB 815 TGGTTGTGTTCTGGTCTGAGCTTCTTCTGGTCAAGCACTATTTCCCTGGAGAAATGCTGT 874  
 QY 881 GGACCAAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGCGAAGAAATCCGGTG 940  
 DB 875 GGGTCAGCTCGTTGAAATCATCAAGTTCTTGGTACACCACTCGAGAGAGATCCGTTG 934  
 QY 941 CATGAACCAAACTACACAGACTTCAGATTCACAAATCAAAAGCCACCCCTTTGGCATAA 1000  
 DB 935 TATGAATCCACACTACACAGACTTTAGGTTCCCGCAGATAAAGGCACATCTTTGGCACA 994  
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 DB 995 GATTTTCCCAAAAGGATCGCTCCAGAGCCATTGATTTTGCATCAAGGCTGCTTCAGTA 1054  
 QY 1061 CTCACCAAGCTACGTTGCACTCGCTCGAGGATGTGCGCATCGGCTTTTCAATGAAT 1120  
 DB 1055 CTCTCAAGCTTAGATGACAGCGCTTGAAGCTTGTGCACATCCGTTCTTGTATGAGCT 1114  
 QY 1121 CGGTGAGCAAAATGCTGCTTCCAAATGGCGACCTCTACACACGTTGTTCAACTTCAA 1180  
 DB 1115 TAGAGAAACCAAAATGCTGCTTTACCAACCGAGCGGCTTTCCCGCGCTCTTCAACTTCAA 1174  
 QY 1181 ACAGAGTTGTCTGGGCTTCCCGGAGCTTATCAACAGCTTAATACAGAGCATGTGAG 1240  
 DB 1175 ACAAGAGGTAGCTGGAGCTTTCACCTGAGCTGGTCAACAAGTTGATTCAGACCATATCAA 1234  
 QY 1241 GGCACAGATGAATGTGGCTTTTCCATTTCAAGCTGGACCCCTAGAAAAGCGATC 1293  
 DB 1235 GACGCAAGTTGGGCTTAAGCTTCTTGAATCAGTCTGGAACCTTAAACAAACGATC 1287  
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 ID ACC57973 standard; cDNA; 1499 BP.  
 XX ACC57973;  
 AC ACC57973;  
 XX DT 11-AUG-2003 (first entry)  
 XX Soybean protein kinase stress-related polypeptide GmPK-1 cDNA.  
 DE GmPK-1; protein kinase stress-related polypeptide; PKSRP; enzyme;  
 XX transgenic plant; plant; stress tolerance; drought tolerance;  
 KW salt tolerance; cold tolerance; soybean; gene; ss.  
 XX Glycine max.  
 XX Key Location/Qualifiers  
 PH CDS 53..1282  
 FT /\*tag= a  
 FT /product= "GmPK-1"  
 XX WO2003040171-A2.  
 XX 15-MAY-2003.  
 PD 12-NOV-2002; 2002WO-US036374.  
 XX

XX 09-NOV-2001; 2001US-0346096P.  
 XX PR (BADI ) BASF PLANT SCI GMBH.  
 XX PA Van Thielien N, Da Costa E SilvaO, Chen R;  
 XX PI WPI; 2003-441522/41.  
 XX DR P-PSDB; ABR42366.  
 XX New protein kinase stress-related polypeptide coding nucleic acid, useful  
 PT for producing transgenic plants with an increased tolerance to an  
 PT environmental stress, e.g. high salinity, as compared to a wild type  
 PT variety of the plant.  
 XX Claim 1; Page 94-95; 111pp; English.  
 XX The present sequence is a full-length cDNA encoding GmpK-1, a novel  
 CC soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was  
 CC identified on the basis of homology to Physcomitrella patens PK-3 (see  
 CC ACC57962) and PK-10 (see ACC57966) sequence. GmpK-1 is an example of  
 CC PKSRPs of the invention that are important for modulating a plant's  
 CC response to environmental stress. Over-expression of PKSRP coding nucleic  
 CC acids in a plant results in the plant's increased tolerance to  
 CC environmental stress. Transgenic monocot and dicot plants are provided  
 CC that show increased tolerance to high salinity, drought and low  
 CC temperature  
 XX Sequence 1499 BP; 431 A; 335 C; 336 G; 397 T; 0 U; 0 Other;  
 SQ  
 Query Match 43.1%; Score 705; DB 8; Length 1499;  
 Best Local Similarity 77.1%; Pred. No. 1.7e-97;  
 Matches 858; Conservative 0; Mismatches 255; Indels 0; Gaps 0;  
 QY 136 CCGATATACACACGACGAAATGCTGCTGCTGTATAGAGAAATGATGCTGTTA 195  
 DB 159 CCGACCGCGGACCGAAAGAAATGTCAGCTCTGTCGACATGTAATGATGACTCA 218  
 QY 196 CCGGTACACATAATTTCTACTACAAATGGAGGCAAAATGGTGAACCTAAACAGACCATTA 255  
 DB 219 CTGGTCACATAATCTCAACCAATTTGACAGGCAAAATGGCGAATCTAAACAAACCATCA 278  
 QY 256 GTTACATGCGCCAAAGTGTGTTGGACAGGATCATTCGGAATTTGATTCAGGCAAAAT 315  
 DB 279 GTTACATGCGCCAAAGTGTGTTGGACAGGATCATTCGGAATTTGATTCAGGCAAAAT 338  
 QY 316 GCTTGGAACTCGAGATTCAGTAGGATTAAGAGGTTTTCAGATGCGCGTTATATAAA 375  
 DB 339 GCTTGGAGACTCGGAGGCGAGTGGCTATTAAGAGGTTTTCAGGACAGGCGGATACAAA 398  
 QY 376 ACCGAGAGTTGCAATTAATCGGACTAATGGACCATCCCAATGTGGTTTCTTTGAAGCAAT 435  
 DB 399 ATCGTGAACCTGAGTTAATGCGGTGATGATCACCACCAATATAATTTCTTGAGTAAT 458  
 QY 436 GTTCTCTCTACAGCACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATATGATAC 495  
 DB 459 ATTCTCTCTCAACAGTAGAGATGAATTTTCTGAACTTTGGTGAATGGAATATGTC 518  
 QY 496 CAGAGACATTTGACCGGTTTGAAGCACTATAGTTTCAACAGCGGATGCGCTATCT 555  
 DB 519 CTGAGACGATCTTCGTTTATTAAGCACTACAGTAGCATGAACAGAGAAATGCCCCCTAA 578  
 QY 556 TCTATGTCAAACTTTACACATACCAAACTTTTCAGAGGCTTTGGCTTATATCCATCTGTC 615  
 DB 579 TCTATGTGAATATATACATATCAATCTTTAGGGACTGGCGTATATCCATCTGATAC 638  
 QY 616 CTGGTGTCTGCCACAGAGATATAAACCAAAATCTTTTGGTTGATCCCAACACCCATC 675  
 DB 639 CAGGAATCTGCCATAGGATTTGAAGCCTTCAAAATCTTTTGGTTGATCGACTCACACACC 698  
 QY 676 AGTGTAAAGCTCTGATTTTGAAGTGAAGTCTGTTGAAGGTTGAAGGTTGAAGGTTGAAG 735  
 DB 699 AAGTCAAGCTCTGATTTTGGAGTGAAGGTTCTGTTGGAGGTTGAATCAAAATTT 758

QY 736 CATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTCCACAGAGTATA 795  
 DB 759 CATACATATGTTACCGGTACTATCGTGGCCAGAGCTAATATTTGGTGGGAGAAATACA 818  
 QY 796 CATCATCCATTGATATATGCTGCTGTTGTTGTTGCTGCGAGAGTACTTCTTTGGGAGC 855  
 DB 819 CACTTCTGTTGATATATTTGGTCCGCTGGTGTGCTTCTTGGGAACTTCTTTAGGCCAGC 878  
 QY 856 CGTTATCCCGGAGAAATTTCTGTGACCACTAGTGGAGATCATAAAGGTTCTTTGGTA 915  
 DB 879 CTTTGTCTCCAGGAGAAATCAGGTTGACCAACTCGTGGAAATTAATCAAGATTCTTTGGCA 938  
 QY 916 CTCCAACTCGGAGAGAAATCCGGTGCATGAACCCAAACTACACAGACTTCAGATTCCCAAC 975  
 DB 939 CTCCTACTCGAGAGAAATTCGATGCATGAATCTCTAATATATACAGATTTCAGATTCCCAAC 998  
 QY 976 AAATCAAGCCACCCCTTGGGATAGGTTTCCCAAGCGGATGCTCCGGAGGCAATG 1035  
 DB 999 ATATCAAGGCTCATCTTGGGATAGGTTTTCACAGGGAATGCTCTCTGAAGCAATG 1058  
 QY 1036 ACCTTGCATCTCGGCTTCTTCAATCACTACCAAGTCTAGCTGCTGCGCTCGAGGCAAT 1095  
 DB 1059 ACCTTGCATCAAGGCTTCTCCAATATTTCCCAAACTTCGTTACAGTGCAGTGGAGCAA 1118  
 QY 1096 GTGCGCATCCGTTTTCATGAATGAATCTCGTGAAGCAAAATGCTGCTTCCAAATGGCCGAC 1155  
 DB 1119 TGGCACAATCTTCTTTCGACGAGCTTCGCGAGCCCAATGCCCGGTACCTAATGCTGCTC 1178  
 QY 1156 CTCTACCAACCGTGTGTTCAACTTCAACAGAGGTTGCTCTGGGGCTTCACGGAGCTTATCA 1215  
 DB 1179 CACTGCTCCCACTTTTCAACTTTAAACAGGAATTAGATGGAGCGCCCTTGAATGCTTTC 1238  
 QY 1216 ACAGCTAATACAGAGCATGTGAGGCGCAGACA 1248  
 DB 1239 CTAAGCTCATCCAGAGCATGTGAGGCGGCAAA 1271  
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 AAC48014  
 ID AAC48014 standard; DNA; 1653 BP.  
 XX AAC48014;  
 XX 18-OCT-2000 (first entry)  
 XX Zea mays DNA fragment SEQ ID NO: 55948.  
 DB Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway; metabolic; pathway;  
 KW promoter; termination sequence; corn; ss.  
 OS Zea mays subsp. mays.  
 XX EP1033405-A2.  
 XX 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-00301439.  
 XX 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126264P.  
 PR 29-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.  
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 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
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 PR 23-APR-1999; 99US-0130510P.

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PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
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PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
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PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
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PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	24-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
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PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
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PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
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PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-01444632P.	PR	14-OCT-1999;	99US-0159637P.





CC 410, 105, 399 or 402 (see ABP53633 to ABP53636) amino acids. (I) is  
 CC useful for immunological screening of cDNA expression libraries, and for  
 CC preparing antibodies against the polypeptides, where the antibodies would  
 CC be useful for detecting (I) in situ or in vitro, in cell extracts.  
 CC Nucleic acids (II) encoding (I) can be used to isolate cDNAs and genes  
 CC encoding homologous proteins from the same or other plant species. (II)  
 CC can also be used for creating transgenic plants in which (I) is present  
 CC at higher or lower levels than normal or in cell types or in  
 CC developmental stages in which they are not normally found. (II) are  
 CC useful as probes or primers. The polynucleotides may be used as probes  
 CC for genetically and physically mapping the genes that they are a part of  
 CC and used as markers for traits linked to those genes. The information can  
 CC be used in plant breeding in order to develop lines with desired  
 CC phenotypes. The present sequence encodes a glycogen synthase kinase from  
 CC the present invention  
 XX  
 SQ Sequence 1673 BP; 419 A; 421 C; 408 G; 424 T; 0 U; 1 Other;  
 Query Match 40.8%; Score 667.2; DB 6; Length 1673;  
 Best Local Similarity 75.3%; Pred. No. 8.3e-92;  
 Matches 831; Conservative 0; Mismatches 273; Indels 0; Gaps 0;  
 QY 145 ACAACGACAAAGAAATGCTGCTGCTGTTATAGAAGGAATGATGTTTACCGGTCA 204  
 DB |||||  
 QY 117 AGAAGCAGCAGATGGCGAGGCGCGTATGCGAGGGGAGACGCGCATGACCGGTCA 176  
 DB |||||  
 QY 205 TAAATTTCTACTAAATGGAGGCAAAATGGTGAACCTTAAACAGACCAATAGTTATCATGG 264  
 DB |||||  
 QY 177 TCATCTCCACCAACCATCGGCGGCAAGACGCGGAGCCCAAGCAGACGATTAGCTACATGG 236  
 DB |||||  
 QY 265 CCGAAGCTGTTGTTGGACAGGATCATTCGGGAATGTTATCCAGGCAAAATGCTTGGAAA 324  
 DB |||||  
 QY 237 CGGAGCGGTTGTGGCACTGCTTGGTGGCATGCTCTTTCAGGCTAAATGCCCTGGAAA 296  
 DB |||||  
 QY 325 CTGGAGATCAGTAGGCATTAAGAAGGTTTGAAGATCGCGCTTATATAAAACCGAGAGT 384  
 DB |||||  
 QY 297 CGGGGAGATGTTGGCATTAGAGAGTACTGCGAGGACAGCGGTACAAGAACCGTGAGC 356  
 DB |||||  
 QY 385 TCAATTAATGCGACTTAATGGACCAATCCAAATGTGGTTTCTTGAAGCAATGTTTCTTCT 444  
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 QY 357 TCGAGCTTATGCTTCGATGATCCATTCATGTTGTTCTCCCTCAAGCACTGCTTCTTCT 416  
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 QY 445 CTACACAGCTAGAGATGAGCTTCTCCTCAATCTCGTTATGAGATATGTACAGAGACAT 504  
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 QY 477 TATACCGGCTGTTAAGCACTACAGTAATGCCAACCGGGGATGCCGTTATCTATGTCA 536  
 DB |||||  
 QY 565 AACTTTACACATACCAAAATCTTTAGAGGCTTGGCTTATATCATATCTGCTCTGGTGTCT 624  
 DB |||||  
 QY 537 AGCTTTACATGATCAGCTTTTATAGAGGCTAGCTTATGTTTCTATCTGTTCCAGGAGTT 596  
 DB |||||  
 QY 625 GCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACCCCATCAGTGTAAAGC 684  
 DB |||||  
 QY 597 GCCACAGGAGATGTAAACCAAAATGTTTGGTTGATCCTCTAAACCCATCAAGTCAAGA 656  
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 QY 685 TCTGTGATTTTGAAGTGAAGTACTGTTGAAGGTTGAACCAACATATCATATATCT 744  
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 QY 657 TCTGTGATCTTTGAAGTGAAGGTTTCTGGTACCTGGTGAACCCCAATAGCATATAT 716  
 DB |||||  
 QY 745 GCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATATCATATCA 804  
 DB |||||  
 QY 717 GCTCTCGCTACTATCGTGTCTCTGAGCTCATATTTGGTGCNACTGAATATACAACTTCAA 776  
 DB |||||  
 QY 805 TTGATATATGCTGCTGTTGTTCTGGCAGAGCTACTTCTTGGGAGCCGTTTATTC 864  
 DB |||||  
 QY 777 TAGACATATGGTCAGCTGGATGTTCTTGCAGAGCTACTTCTTGGTCAAGCTCTGTTTC 836  
 DB |||||  
 QY 865 CGGGGAAATTTCTGTGGACAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCAACTC 924  
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 QY 837 CAGGAGAGACTCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGGTACTCCAAACC 896  
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Search completed: June 23, 2005, 11:46:58  
 Job time : 1289.09 secs

QY 925 GCGAAGAAATCGGTGCTGATGAACCCAAACTACAGACTTCAGATTCCACAAATCAAG 984  
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 QY 897 GTGAGAAATTCGGTGCATGAACCCCAACTATACCGAGTTTCAGGTTTCTCAGATTAAAGG 956  
 DB |||||  
 QY 985 CCCACCTTTGGCATAAAGGTTTTCCACAAGCGGATGCTCCCGAAGCCATTGACCTTGCA 1044  
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 QY 1017 CCCGCTTTCTCCAGTATTCCAAATCTACGTTGCACTGCTCTTGTATGATGTGCACATT 1076  
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 QY 1105 CGTTTTCAATGAATCTCGTGAGCCAAATGCTGCTTCCAAATGGCGGACCTCTACCA 1164  
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 QY 1077 CTTCTTTGATGAGCTACGTGAGCGCAATGCACTGCTGCGAATGGCGCCCATTTCCCTC 1136  
 DB |||||  
 QY 1165 CGTTGTTCAACTTCAAAACAAGATTTGCTGGGGCTTACCGGAGCTTATCAACAGGCTAA 1224  
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 QY 1137 CTCGTTTCACTTCAAACTGAATAGCGAAGCGCTCTCCAGAGCTCATCAACAGGCTTG 1196  
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 QY 1197 TTCCGGRACATGTTCCGACGCAAA 1220  
 DB |||||

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:21:17 ; Search time 397.52 Seconds  
(without alignments)  
6734.116 Million cell updates/sec

Title: X94938  
Perfect score: 1636  
Sequence: 1 TTTACTCTTTCAGTCAGAGA.....AAAAAAAAAAAAAAAAAAAA 1636

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1636	100.0	1636	4	US-09-578-194-6
2	667.2	40.8	1673	3	US-09-347-801-15
3	667.2	40.8	1673	3	US-09-854-731-15
4	557.2	34.1	1814	3	US-09-347-801-9
5	557.2	34.1	1814	4	US-09-854-731-9
6	538.8	32.9	1429	3	US-09-347-801-13
7	538.8	32.9	1429	4	US-09-854-731-13
8	400.8	24.5	1952	4	US-09-566-921-24
9	400.8	24.5	1952	3	US-09-488-856A-3
10	395.6	24.2	1389	3	US-09-489-765A-3
11	395.6	24.2	1389	4	US-09-016-434-1414
12	394	24.1	2088	2	US-08-602-264A-1
13	394	24.1	2088	3	US-08-461-018A-1
14	394	24.1	2088	3	US-09-216-958-1
15	390	23.8	1972	2	US-08-602-264A-2
16	390	23.8	1972	3	US-09-216-958-2
17	390	23.8	1972	3	US-08-461-018A-2
18	289.6	17.7	1185	4	US-09-248-796A-4396
19	174.2	10.6	304	4	US-09-313-294A-6825
20	154	9.4	286	4	US-09-313-294A-6825
21	140.2	8.6	305	4	US-09-313-294A-5874
22	134.6	8.2	1236	4	US-09-248-796A-4397
23	122.6	7.5	584	3	US-09-347-801-11
24	122.6	7.5	584	4	US-09-854-731-11
25	106.4	6.5	275	4	US-09-313-294A-1703
26	101.6	6.2	472	4	US-09-313-294A-6721
27	96.2	5.9	479	2	US-08-602-264A-13

28	96.2	5.9	479	3	US-08-461-018A-13	Sequence 13, Appl
29	96.2	5.9	479	3	US-09-216-958-13	Sequence 13, Appl
30	94.6	5.8	2447	2	US-09-014-969-14	Sequence 14, Appl
31	93.6	5.7	1474	3	US-08-821-994-64	Sequence 64, Appl
32	93.4	5.7	441	4	US-09-601-537-10	Sequence 10, Appl
33	93.4	5.7	4121	4	US-09-601-537-9	Sequence 9, Appl
34	92.8	5.7	1882	3	US-09-370-253-1	Sequence 1, Appl
35	92.6	5.7	1342	4	US-09-489-847-89	Sequence 89, Appl
36	91.8	5.6	1771	4	US-09-907-794A-158	Sequence 158, Appl
37	91.8	5.6	1771	4	US-09-866-028-36	Sequence 36, Appl
38	91.8	5.6	1771	4	US-09-905-125A-158	Sequence 158, Appl
39	91.8	5.6	1771	4	US-09-902-775A-158	Sequence 158, Appl
40	91.8	5.6	1771	4	US-09-906-700-158	Sequence 158, Appl
41	91.8	5.6	1771	4	US-09-944-457-36	Sequence 36, Appl
42	91.8	5.6	1771	4	US-09-903-603A-158	Sequence 158, Appl
43	91.8	5.6	1771	4	US-09-904-920A-158	Sequence 158, Appl
44	91.8	5.6	1771	4	US-09-909-064-158	Sequence 158, Appl
45	91.8	5.6	1771	4	US-09-905-381A-158	Sequence 158, Appl

## ALIGNMENTS

RESULT 1  
US-09-578-194-6  
; Sequence 6, Application US/09578194  
; Patent No. 6822139  
; GENERAL INFORMATION:  
; APPLICANT: Sudwestdeutsche Saatzaucht-SWS  
; APPLICANT: Advanta Seeds B.V.  
; TITLE OF INVENTION: Modulation of Storage Organs  
; FILE REFERENCE: 026-1  
; CURRENT APPLICATION NUMBER: US/09/578.194  
; CURRENT FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1636  
; TYPE: DNA  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: mRNA  
; LOCATION: (1)..(1636)  
; OTHER INFORMATION: strain Columbia ecotype  
; OTHER INFORMATION: taxon:3702  
; OTHER INFORMATION: tissue type leaves  
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots  
; PUBLICATION INFORMATION:  
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lechamy, A. and Kreis, M.  
; TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)  
; TITLE: from Arabidopsis thaliana ( Accession No. 6822139 X94938, x94939 and X99696)  
; TITLE: (008)  
; JOURNAL: Plant Physiol.  
; VOLUME: 113  
; ISSUE: 1  
; PAGES: 306-306  
; DATE: 1997-01-01  
; DATABASE ACCESSION NUMBER: genbank/X94938  
; DATABASE ENTRY DATE: 1998-02-13  
; RELEVANT RESIDUES: (1)..(1636)  
US-09-578-194-6

Query Match 100.0%; Score 1636; DB 4; Length 1636;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTACTCTTTCAGTCAGAGAGAGTTAGAGCTGTAAAGCATGATCTTCGATACCAT 60

Db 1 TTTACTCTTTCAGTCAGAGAGAGTTAGAGCTGTAAAGCATGATCTTCGATACCAT 60

Qy 61 TGGGGCTCTTCAGCTCCGCTTTTAGCTCTTCAGCCCGCCGATCTTCACGCGGAGATT 120

Db 61 TGGGGCTCTTCAGCTCCGCTTTTAGCTCTTCAGCCCGCCGATCTTCACGCGGAGATT 120

= instant  
Case



Qy	325	CTGGAAATCAGTAGCCATTAAGAAGAGTTTTCGAAGATGCCGTTTATATAAAACCGAGAGT	384
Db	297	CCGGGAGATGGTGGGCATTAAGAAGAGTACTGCAAGACAGACGGTACAAGAACCGTGAGC	356
Qy	385	TGCAATTAATCGACTAATGAGCAATCCAAATGTGTTTCCTTGAAGCATTTGTTCTTCT	444
Db	357	TGCAGCTTATGGGTTGATGATCCATTCOAATGTTGTCTCCCTCAAGCACTGCTTCTCT	416
Qy	445	CTACAACGACTAGAGATGAGCTCTTCCTCAATCTCGTTATGAGGATGTATGACAGAGACAT	504
Db	417	CAACCAAGTAGAGATGAGCTGTTTCTTGAACTTGTCATGAGTATGTCCCGGAGACGC	476
Qy	505	TGTACCGGGTTTGAAGCACTATAC TAGTTCAAACGAGGATGCTATCTTCTATGTCA	564
Db	477	TATACCGGTGCTTAAGCACTACAGTAAATGCCAACGAGGGATGCGCTTATCTATGTCA	536
Qy	565	AACTTTACACATACCAAATCTTCAGAGCGTTGGCTTATATCCATACCTGCTCGTGTGCT	624
Db	537	AGCTTTACATGTATCAGCTTTTAGGGGCTAGCTTATGTTCATACTGTTCCAGGAGTTT	596
Qy	625	GCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCCACACCCATCAGTGTAAAGC	684
Db	597	GCCACAGGATGTGAAACCAAAATGTTTGGTTGATCTCTAACCCCATCAAGTCAAGA	656
Qy	685	TCTGTGATTTTGAAGTGCAAAAGTACTGTGTGAAAGGTGAACAAACATATCATATATCT	744
Db	657	TCTGTGACTTTGGAAGTGCAAAAGTTCTGGTACCTGGTGAACCCAAACATAGCATACATAT	716
Qy	745	GCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGGCCACAGAGTATACATATCCA	804
Db	717	GCTCTCGCTACTATCGTGCTCTCGAGCTCATATTTGGTGCAACTGAATATACACTTCAA	776
Qy	805	TTGATATATGTTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTGGGCAAGCGTTATTCC	864
Db	777	TAGACATATGTTCACTGATGTTCTTTCGACAGAGCTACTTCTTGGTCAGCCCTCTGTTTC	836
Qy	865	CGGAGAAATTTCTGTGACACGCTAGTGTGAGATCATTAAGGTTCTTGGTACTCAACATC	924
Db	837	CAGGAGAGACTGCGGTTTGATCAGCTTAGTGGAGATTAACAAGGTTCTTGGTATCCCAACC	896
Qy	925	GCGAAGAAATCCGGTGCATGAACCCAACTACACAGACTTCAGATTCCACAAATCAAG	984
Db	897	GTGAGGAAATTCGGTGCATGAACCCCAACTATACCGAGTTCAAGGTTCTTCAGATTAGG	956
Qy	985	CCCACCTTTGGCATAAGGTTTTCACAAACGCGATGCCTCCGGAAGCCATTGACCTTGAT	1044
Db	957	CTCATCTTTGGCAACAAGATTTTCACAAAGAAATGCCCGCTGAAGCTATAGATCTTGCT	1016
Qy	1045	CTCGGCTTCTTCAATATCTCAACAAGCTTAGTTGCACTGCGGCTCGAGGCAATGTGCGCATC	1104
Db	1017	CCCGCTTCTCGATTAATTCACAAATCTACGTTGCATGCTCTCTTGATGATGTGCACATT	1076
Qy	1105	CGTTTTTCAATGAACTCCGTGAGCAAAATGTCGTTCTTCCAAATGGCGCACTCTACCAAC	1164
Db	1077	CTTCTTTGATGAGCTACGTGAGCCGAATGACGCTTGCCGAATGGCGCCCATTTCCCTTC	1136
Qy	1165	CGTTGTTCAAATTCAAAACAAGATTGTTCTGGGGCTTCCACCGAGCTTATCAACAGGCTAA	1224
Db	1137	CTCTGTTCAAATTCAAACCTGAACTAGCGAAGCCCTCTCCAGAGCTCATCAACAGGCTTG	1196
Qy	1225	TACAGAGCATGTGAGGCGACAGA	1248
Db	1197	TTCCGGAAATGTTTCGAGGCAAA	1220

### RESULT 3

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US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases

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Db 897 GTGAGGAATTCGGTCATGAACCCCACTATACCGAGTTCAGGTTTCCTCAGATTAAGG 956  
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Db 957 CTCATCTTTGGCAAGAATTTTCCACAGAGAAATGCCCGCTGAAGCTATAGATCTTGCCT 1016  
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Qy 1105 CGTTTTTCAATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGCGCCGACCTCTACCCAC 1164  
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Qy 1165 CGTTGTTCAACTCAACAGAGTTGTCTGGGCTTCAACCGGAGCTTATCAACAGGCTAA 1224  
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Db 1197 TTCGGAACATGTTGACGGCAAA 1220

RESULT 4  
US-09-347-801-9  
; Sequence 9, Application US/09347801  
; Patent No. 6262345  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; EARLIER FILING DATE: 1999-07-02  
; EARLIER FILING DATE: 60/092,438  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 1814  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-347-801-9

Query Match 34.1%; Score 557.2; DB 3; Length 1814;  
Best Local Similarity 70.9%; Pred. No. 2.4e-116;  
Matches 739; Conservative 0; Mismatches 303; Indels 0; Gaps 0;  
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Qy 201 CACATAATTTCTACTACAATTTGGAGCAAAATGGTGAACCTTAAACAGACCATTTAGTTAC 260  
Db 393 CATATCATGTGACCACTGATGGAGAAATGGGCGAGCAAGCAGACCATTTAGTTAC 452  
Qy 261 ATGGCCGAACGTGTTGTTGAACAGAGATCAATTCGGAATGTTATTCAGGCAAAATGCTTG 320  
Db 453 ATGGCTGAGCGGTGGTGGTCTGAGTCTGCGAACCGTTTTTCCAGGCGCAAGTGTCTT 512  
Qy 321 GAACTCGGAAATCAGTAGCCATTTAAGAAGGTTTTCAGAGTCCCGTTTATAAAACCGA 380  
Db 513 GAACTGGTAGCCGTGATCTATAAAAGGTTCTTCAAGCAGAGATCAAGATCGT 572  
Qy 381 GAGTTCAAATTAATGCGACTAATGGACCATCCAAATGTGTTTCTTTGAAGCATTTGTTTC 440  
Db 573 GAGTGCAAACCATGCGAGTGTGACCAACCAAAATGTGGTGTCTTAAAGCATGTTTC 632  
Qy 441 TTCTCTACAGACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATGATACACGAG 500  
Db 633 TTCTCAAAGACTGAGAAAGAGGAGCTTTACCTCAATTTGGTGTCTGTGATGTATGCCGAG 692

Qy 501 ACATTGTATCCGGTTTTGAAGCACTATATCTAGTTTCAAAACCGGATGCTATCTTCTAT 560  
Db 693 ACTGCTCATCGTGTCTATCAAAATTTACAACAGATGAACCGCATGCTTTGATTAT 752  
Qy 561 GTCAAACTTTACATACCAAAATCTTCAGAGCTTTGGCTTTATATCCATCTCTCTCTGT 620  
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Qy 621 GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGTATCCCAACCCATCAGTGT 680  
Db 813 GTGTGCCACAGGACATTAAGCCGCAAAATCTCTGGTTAAATCCTCATACCCATCAGTAA 872  
Qy 681 AAGCTCTGTGATTTTGGAGAGTCAAAAGTACTTGGTCAAGAGTGAACCAACATATCATAT 740  
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Db 933 ATCTGTTCTAGTACTTACAGAGCTCCAGAGCTCATATTTTGGTGCTACTGAATACACAACA 992  
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Qy 921 ACTCGGAAAGAAATCCGGTGCATGAACCCAACTACACAGACTTCAGATTTCCACAAATC 980  
Db 1113 ACACGTGAAGAAATTAAGTGCATGAATCCAAATTTATCCGAGTTTAAATTTCCGCAAAATC 1172  
Qy 981 AAAGCCCACTTGGCATAAGGTTTCCACAGCGAGTCCCTCCGAGCCATTTGACCTT 1040  
Db 1173 AAAGTCAACCCATGCAAGATATTTCCATAAAGATGCTGCTGAGCGGTAGATCTC 1232  
Qy 1041 GCATCTCGGCTTCTTCAATACTCACCAGTCTACGTTGCACTGCGCTCGAGGATGTGCG 1100  
Db 1233 GTGTCCAGGCTTCTGCACTACTCACCAGTCTTCCGCTGCTGCTGCTGCTGCTGCTG 1292  
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Qy 1161 CCACGCTGCTTCAACTTCAAC 1182  
Db 1353 CCGCTCTCTTCAATTTAAGC 1374

RESULT 5  
US-09-854-731-9  
; Sequence 9, Application US/09854731  
; Patent No. 6794561  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 1814  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-854-731-9

Query Match 34.1%; Score 557.2; DB 4; Length 1814;  
Best Local Similarity 70.9%; Pred. No. 2.4e-116;  
Matches 739; Conservative 0; Mismatches 303; Indels 0; Gaps 0;





QY 1048 GCGTCTTCAATACCAAGTCTACGTTGCACTGCGCTGAGGATGTGGGATCCGT 1107  
 Db 1123 GACTACTCAATACCTCCCTAACTTGGCGTGACAGTTTATAGATCCCTTGGACGACCCCT 1182  
 QY 1108 T---TTTCAATCAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGCGGACCTCTTACCAC 1164  
 Db 1193 TTCCTTTGGAGCAATTCGNGATCCAAATCTTCGCTTGGCAATGGCGGATCCNTCAA 1242  
 QY 1165 CGTGTCTCAACTTCAACAA 1184  
 Db 1243 CAACTATTAAATCAAAACCA 1262

RESULT 8

US-09-566-921-24  
 ; Sequence 24, Application US/09566921  
 ; Patent No. 6682888  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loring, Jeanne F.  
 ; APPLICANT: Tingley, Debora W.  
 ; APPLICANT: Edwards, Carla M.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE  
 ; FILE REFERENCE: PA-0024 US  
 ; CURRENT APPLICATION NUMBER: US/09/566,921  
 ; CURRENT FILING DATE: 2000-05-05  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 24  
 ; LENGTH: 1952  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. 6682888 234735.15  
 US-09-566-921-24

Query Match 24.5%; Score 400.8; DB 4; Length 1952;  
 Best Local Similarity 63.2%; Pred. No. 5.5e-81;  
 Matches 650; Conservative 0; Mismatches 372; Indels 6; Gaps 2;

QY 217 CAATTGGAGGCAAAATGGTGAACCTTAACAGACATTAGTTACATGCGCGCACTGTTG 276  
 Db 204 CCACTCTAGGCGAAGCCAGAGCGCTCCCAAGAGTGGCTTACACGACATCAAGTGA 263  
 QY 277 TTGGAACAGGATCATTTGGCAATTTGTTCCAGGCAAAATGCTTGAAGTGGAGAACTGAGAACTCAG 336  
 Db 264 TTGGCAATGGCTCATTTGGGTCGTGTACAGGCAAGGCTGGCAGAGACCGAGGACTAG 323  
 QY 337 TAGCCATTGAAGAGTTTGGCAAGATCCCGTTATPAAACCGAGAGTTGCAATTAATGC 396  
 Db 324 TCGCCATCAAGAAGTTCTCCAGGACAAGAGTTTCAAGAACCGAGAGCTGCAGATCATGC 383  
 QY 397 GACTAATGGACCATCAATATGTTTCTTCTTGAAGCATGTTTCTTCTC---TACACGA 453  
 Db 384 GTAAGCTGGACCATGCAATATTTGAGGCTGAGATACCTTTTCTACTCCAGTGGCGAGA 443  
 QY 454 CTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACAGAGACATTGTACCGGG 513  
 Db 444 AGAAGAGAGGCTTTACCTAAATCTGGTGGATATGTGCGCGAGACAGTGTACCGGG 503  
 QY 514 TTTTGAAGCATTACTACTAGTTTCAACACCGAGATGCTTATCTTATGTCAAACTTTACA 573  
 Db 504 TGGCCCGCCACTTCAACCAAGGCAAGTTGACCATCCCTATCTCTATGTCAAGGTGTACA 563  
 QY 574 CATACCAATCTTACAGAGCTTGGCTTATATCACTACTGCTCTGCTGCTGCGACAG 633  
 Db 564 TGTACAGCTCTTCCGAGCTTGGCCTACATCCA---CTCCCGAGGCGGTGTGTACACCGC 620  
 QY 634 ATATAAACCAAAATCTTTTGGTTGATCCCAACCCCATCAGTGAAGCTCTGTGATT 693  
 Db 621 ACATCAAGCCCAAGAACCTGCTGGTGGACCTTGACACATGCTGTCTCAAGCTCTGCGATT 680

QY 694 TTGGAAGTGCAAAAGTACTGGTGAAGGTGAACCAACATATATATATCTCTCTCGT 753  
 Db 681 TTGGAGTGCAAAAGCAGTTGGTCGAGGGGAGCCCAATGTCTCTTACATCTGTCTCTCGT 740  
 QY 754 ATTACCGAGCTCCAGAACTCATCTTTGGTGGCAGAGATATACATCATCTCATTTGATATAT 813  
 Db 741 ACTACCGGCGCCAGAGCTCATCTTTGGAGCAGATGATTAACCTCATCTCATCTGATGTT 800  
 QY 814 GGTCTGCTGGTGTGTTCTTGGCAGAGTACTTCTTGGGAGCGCGTATTTCCCGGAGAAA 873  
 Db 801 GGTCAAGCTGGCTGTACTGGCAGAGCTCTCTTGGGCGAGCCCATCTTCCCTGGGACA 860  
 QY 874 ATTCTGTGACAGCTAGTGGAGATCAAAAGTCTTGGTACTTCAACTCGGAGAAA 933  
 Db 861 GTGGGTGGACAGCTGGTGGAGATCATCAAGGTGCTGGGAAACACCAACCCCGGAAACAA 920  
 QY 934 TCCGCTGATGAACCCAACTTACAGAGATTCAGATTCACCAAAATCAAAAGCCCAACCTT 993  
 Db 921 TCCGAGAGATGAACCCCAACTTACAGGAGTTCAAGTTCCTCAGATTAAAGCTCACCTT 980  
 QY 994 GGCATAAGGTTTCCCAAGCGGATGCTTCCGGAAGCCATTGACCTTGCATCTCGGCTTC 1053  
 Db 981 GGACAAAGGTGTTCAAAATCTCGAAGCGCGCAGAGGCCATCGCGCTCTGCTCTAGCCTGC 1040  
 QY 1054 TTCAATACTACCAAGTCTAGTTGCACTGGCTCGAGGATGCGGATCGGTTTTC 1113  
 Db 1041 TGGAGTACACCCCATCTTCAAGGCTCTCCCACTAGAGGCTGTGCGACAGCTTCTTTG 1100  
 QY 1114 ATGAACCTCGTGAGCCAAATGCTGTCTTCAAAATGGCGGACCTTACACCGTTGTTCA 1173  
 Db 1101 ATGAACCTCGATGTCTGGGAACCCAGCTGCTTAACACCGGCCACTTCCCTCTCTTCA 1160  
 QY 1174 ACTTCAAAACAGAGTTGTCTGGGCTTCCCGGAGCTTATCAACAGGCTTAATACAGAGC 1233  
 Db 1161 ACTTCAGTGTGGTGAACCTCTCCATCAACCGCTCTCTCAACGCCATTTCTATCCCTCTC 1220  
 QY 1234 ATGTGAGG 1241  
 Db 1221 ACTTGAGG 1228

RESULT 9

US-09-488-856A-3  
 ; Sequence 3, Application US/09488856A  
 ; Patent No. 6316259  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; APPLICANT: Robert McKay  
 ; APPLICANT: Madeline M. Butler  
 ; APPLICANT: Jacqueline Wyatt  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP  
 ; FILE REFERENCE: RTS-0115  
 ; CURRENT APPLICATION NUMBER: US/09/488,856A  
 ; CURRENT FILING DATE: 2000-01-21  
 ; NUMBER OF SEQ ID NOS: 88  
 ; SEQ ID NO 3  
 ; LENGTH: 2154  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (92)... (1543)  
 US-09-488-856A-3

Query Match 24.5%; Score 400.8; DB 3; Length 2154;  
 Best Local Similarity 63.2%; Pred. No. 5.6e-81;  
 Matches 650; Conservative 0; Mismatches 372; Indels 6; Gaps 2;

QY 217 CAATTGGAGGCAAAATGGTGAACCTTAACAGACATTAGTTATAGTTCGCGAAGCTGTTG 276  
 Db 405 CCATCTAGGCGCAAGGCCAGAGCGCTCCCAAGAGTGGCTTACACGACATCAAGTGA 464  
 QY 277 TTGGAACAGGATCATTCGGAATGTATTTCCAGGCAAAATGCTTGGAAACTCGGAGAACTCAG 336

Db 465 TTGGCAATGGCTCATTTTGGGTCGTGTACCGACCGCTGGCAGAGACCGGGAACCTAG 524  
QY 337 TAGCCATTAAAGAGTTTTCGAAGATCGCGGTTATATAAAACCGAGAGTTGCAATTAATCC 396  
Db 525 TCGCCATTCAAGAGTTTCTCCAGGACAAGAGTTTCAAGAACCGGAGAGCTGCGAGATCATCC 584  
QY 397 GACTAATGACCATCCAAATGTTGTTTCTTGAAGCATTTTCTTCTC- --TACAACA 453  
Db 585 GTAAGCTGGACCACTCAATATTTGAGGCTGAGATACCTTTTCTACTCCAGTGGCGAGA 644  
QY 454 CTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATGATGTACAGAGACATTTGTACCGGG 513  
Db 645 AGAAGACGAGCTTTTACCTAAATCTGTGCTGGAATATGTGCCGAGACAGTGTACCGGG 704  
QY 514 TTTTGAAGCATTACTAGTTCAACACGAGGATGCTATCTTCTATGTCGAACTTTTACA 573  
Db 705 TGGCCCGCCACTTCAACCAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAGGTGTACA 764  
QY 574 CATACCAAAATCTTCAGAGCTTGGCTTTATATCCATACCTCTCTGTGTCTGCCACAGAG 633  
Db 765 TGTACAGCTCTTCCGAGCTTGGCTTACATCA- --CTCCAGGCGGTGTACCGCG 821  
QY 634 ATATAAAACCAAAATCTTTTGGTTGATCCCCACACCCCATCAGTGTAAAGCTCTGTGATT 693  
Db 822 ACATCAAGCCCCAGAACCTGTGTTGGACCCCTGACACTGTGTCTCAAGCTCTGCGATT 881  
QY 694 TTGGAAGTGCMAAGTACTGTGTGAAGGTGAACCAAAATATCATATATCTGCTCTCGGT 753  
Db 882 TTGGCAGTGCMAAGCAGTTGGTCCGAGGGAGGCCAAATGTCTCTACATCTGTCTCGCT 941  
QY 754 ATTACCGAGCTCCAGAACTCATCTTTTGGTGCACAGAGTATACATCATCATTTGATATAT 813  
Db 942 ACTACCGGGCCCAGAGCTCATCTTTTGGAGCCACTGATTACACTCATCATCGATGTTT 1001  
QY 814 GGTCTCTGTGTGTCTGGCAGAGCTACTTCTTGGGCGAGCGGTTATTTCCCGGGAGAAA 873  
Db 1002 GGTCACTGGCTGTGTACTGGCAGAGCTCTCTTGGGCGAGCCCATCTTCCCTGGGGACA 1061  
QY 874 ATTCTGTGACCAAGCTAGTGGAGATCATTAAGGTTCTTGGTACTCCAACTCGGGAAGAAA 933  
Db 1062 GTGGGTTGGACCAAGCTGTGGAGATCATCAAGGTGTGGGAAACCAACCCCGGGAAACAAA 1121  
QY 934 TCCGTTGTCATGAACCAACTACACAGACTTCAGATTTCACAAATCAAAAGCCACCCCTT 993  
Db 1122 TCCGAGAGTGAACCCCAACTACACGAGTTCAAGTTCCCTCAGATTAAGCTCACCCCT 1181  
QY 994 GGCATAAGGTTTTCACAAAGCGGATGCCTCCGGAAGCCATTGACCTTCGATCTCGGCTTC 1053  
Db 1182 GGACAAAGGTTTCAAATCTCGAAACGCGCCAGAGGCCATCGCGCTCTGCTCTAGCCTGC 1241  
QY 1054 TTCAATACTCACCAAGTCTAGTTGCACTGCGCTCGAGGATGTGGCATCGGTTTTCAT 1113  
Db 1242 TGGAGTACACCCCATCTCTCAAGGCTCTCCCACTAGAGGCGCTTGGCGCACAGCTTCTTTG 1301  
QY 1114 ATCAACTCCGTGAGCCAAATGCTCTTCCAAATGGCGACCTCTACACACCGTTGTTCAT 1173  
Db 1302 ATGAATCTGCATGTCTGGGAACCCAGCTGCTTAAACCGCCCACTTCCCTCTCTTCA 1361  
QY 1174 ACTTCAAAACAAAGATTGTCTGGGGCTTTCACCGGAGCTTATCAACAGGCTTAATACAGAGC 1233  
Db 1362 ACTTCAGTGTGTGAACCTCTCCATCCAAACCGTCTCTCAAGCCATTTCTCATCCCTCCTC 1421  
QY 1234 ATGTGAGG 1241  
Db 1422 ACTTGAGG 1429

RESULT 10  
US-09-489-765A-3  
; Sequence 3, Application US/09489765A  
; Patent No. 6323029  
; GENERAL INFORMATION:

; APPLICANT: Madeline M. Butler  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION  
; FILE REFERENCE: RTS-0124  
; CURRENT APPLICATION NUMBER: US/09/489,765A  
; CURRENT FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 3  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)...(1302)  
US-09-489-765A-3

Query Match 24.2%; Score 395.6; DB 3; Length 1389;  
Best Local Similarity 65.6%; Pred. No. 7.3e-80;  
Matches 610; Conservative 0; Mismatches 314; Indels 6; Gaps 2;  
QY 253 TTAGTTACATGCGCCGAAAGTGTGTTGGAAACAGGATCATTCGGAATTTGATTTCCAGGCAA 312  
Db 200 TCAGCTATACAGACACTAAAGTGATTGGAATGGAATCATTTGGTGTGTATATCAAGCCA 259  
QY 313 AATGCTTGGAACTCGAGAAATCAGTAGCCATTAAAGAGGTTTTCGAAAGATCGCGTTATA 372  
Db 260 AACTTTGTGATTTCAGAGAACTGGTGCCTCAAGAAAGTATTCAGGACAAGATTTTA 319  
QY 373 AAAACCGAGAGTTGCAATTAATGCGACTAATGGAACCATCCAAATGTGTTTCTTCTTGAAGC 432  
Db 320 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCGATT 379  
QY 433 ATGTTTCTTCTC- --TACAACGACTAGAGATGAGCTCTTCTCTCAATCTCTGTTATGAGAT 489  
Db 380 ATTCTCTTCTACTCCAGTGGTGAGAAAGAGTGTATCTTAACTCTGTTGCTGAGACT 439  
QY 490 ATGTACACGAGAGATTGTACCGGTTTGAAGCACTATATAGTTTCAACACGAGCGATGC 549  
Db 440 ATGTTCCGGAACAGTATACAGAGTTGCCAGACACTATAGTCAGGCCAACAGACGCTCC 499  
QY 550 CTATCTTCTATGTCAAACTTTACACATACCAATCTTCAGAGGCTTGGCTTATATCCATA 609  
Db 500 CTGTGATTATGTCAAGTTGTATATGTATCAGCTGTTCGGAAGTTTAGCTATATCCA- -- 557  
QY 610 CTGCTCTGCTGTGCGCACAGAGATATAAAACCAACCAAAATCTTTTGGTTGATCCCCACA 669  
Db 558 -TTCCCTTTGGAATCTGCCATCGGGATATTAAACCGCAGAAACCTCTTTTGGATCCCTGATA 616  
QY 670 CCCATCAGTGTAGCTCTGTGATTTTGGAAAGTGCAAAAGTACTGTGTGAAGGTGAACCAA 729  
Db 617 CTGCTGTATTAACACTCTGTGACTTTTGGAAAGTGCAAAAGCAGCTGTGTCGAGGAAACCCA 676  
QY 730 ACATATCATATATCTGCTCTCGGTATTCAGAGCTTCAGAACTCATCTTTTGGTGCACAG 789  
Db 677 ATGTTTGTGATATCTGTTCTCTGCTACTATAGGSCACACAGAGTTGATCTTTTGGAGCCACTG 736  
QY 790 AGTATACATCATCCATTGATATATGCTCTGCTGTTGTTGTTCTTGGCAGAGCTACTTCTTG 849  
Db 737 ATTATACCTCTAGTATAGATGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAG 796  
QY 850 GGCAGCGGTTATTTCCCGGAGAAATTTCTGTGGACCGAGCTAGTGGAGATCATATAAGGTTTC 909  
Db 797 GACAAACAATATTTCCAGGGATAGTGGTGTGGATCAGTTGGTAGAAATATCAAGGTCC 856  
QY 910 TTGGTACTCCAACTCGCGAAGAAATCCGGTGCATGAACCCAACTACACAGACTTCAGAT 969  
Db 857 TGGGAATCCCAACAGGAGGCAAAATCAGAGAAATGAACCCAACTACACAGAAATTTAAAT 916  
QY 970 TCCCAAAATCAAGCCCAACCTTGGCATAGAGTTTTCACAGCGGATGCTCTCCGGAAG 1029  
Db 917 TCCCTCAAAATTAAGGCACATCTCTTGGACTTAAGGTCTTTCGAGCCCGGAGG 976



QY 1030 CCATTGACCTTGCATCTCGGCTTCTTCAATCTACCAAGTCTACGTTGCCACTGGCTCG 1089  
DB 977 CAATTGCACTGTGTAGCCGTCTGCTGGAGTATACACCAACTGCCGCACTTAAACCACTGG 1036  
QY 1090 AGGCATGTCGCATCGTTTTCATGAAGTCTCGTGAGCCAAATGCTCGTCTTCCAAATG 1149  
DB 1037 AGCTTGTGCATCATTTTGTGATGATTAAGGACCCAAATGTCAAAATCCAAATG 1096  
QY 1150 GCCGACCTCTACCAAGCTGTTCACACTTCA 1179  
DB 1097 GCGGAGACACACCTGCACCTTCAACTTCA 1126

## RESULT 11

US-09-016-434-1414  
; Sequence 1414, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1414:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1389 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9529236

## US-09-016-434-1414

Query Match 24.2%; Score 395.6; DB 4; Length 1389;  
Best Local Similarity 65.6%; Pred. No. 7.3e-80;  
Matches 610; Conservative 0; Mismatches 314; Indels 6; Gaps 2;  
QY 253 TTAGTTACATGCCGCAAGCTGTGTGTTGGAACAGGATCAATTCGGAATGTATTCCAGGCAA 312  
DB 200 TCAGCTATACAGACACTAAAGTGAATGGAATGATCATTTGGTGTGTATATCAAGCCA 259  
QY 313 AATGCTTGGAACTCGAATCAGTAGCCATTAAGAGGTTTGGCAAGTCCGCTTATA 372  
DB 260 AACTTGTGATTCAGGAGAACTGGTCGCCATCAAGAAAGTATTGCAAGCAAGAGATTTA 319

QY 373 AAAACCGAGAGTTGCAATTAATGCGACTTAATGAGACCATCCAAATGTGGTTTCTTGTGAAGC 432  
DB 320 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTCCGATTTGCGGTT 379  
QY 433 ATTGTTTCTTCTC---TACACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGT 489  
DB 380 ATTTCTTCTTACTCCAGTGGTGAGAAAGATGAGGTCTATCTTAATCTGGTGGCTGGACT 439  
QY 490 ATGTACAGAGACATTTGTACCGGGTTTGAAGCACTATATACTAGTTCAAACACGAGCGATGC 549  
DB 440 ATGTTCCGGAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCC 499  
QY 550 CTATCTTCTATGTCAAACCTTTACACATACCAAACTTTCCAGAGCTTGGCTTATATCCATA 609  
DB 500 CTGTGATTTATGTCAAAGTTGTATATGATGATCTGCGAAGTTTAGCCTATATCCA-- 557  
QY 610 CTGCTCTGCTGTCGCCACAGAGATATAAAACCAACCAAAATCTTTTGGTGTGATCCCCACA 669  
DB 558 -TTCTTTTGAATCTGCCATCGGATATTAACCCGAGAACCTCTTGTGGATCCTGATA 616  
QY 670 CCCATCAGTGAAGCTCTGTGATTTTGAAGTGCAAAAGTACTGTGAAAGGTGAACCAA 729  
DB 617 CTGCTGTATTAAGACTCTGTGACTTTTGAAGTGCAAAGCAGCTGTCCGAGAGAACCCA 676  
QY 730 ACATATCATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGGCCACAG 789  
DB 677 ATGTTTCGTATATCTGTTCTCGGTACTATAGGGCACACAGAGTTGATCTTTGGAGCCACTG 736  
QY 790 AGTATACATCATCCATTTGATATATGTTGCTGCTGGTGTGTTCTGCGAGAGCTACTTCTTG 849  
DB 737 ATTATACCTCTAGTATAGATGTATGCTGCTGGCTGTGTGTTGGCTGAGCTGTACTAG 796  
QY 850 GCGAGCCGTTATTCGCCGGAGAAATTTCTGGGACAGCTAGTGGAGATCATAAAGGTTTC 909  
DB 797 GACAAACCAATATTTCCAGGGGATAGTGTGTGGATCAGTTGGTAGAATATATCAAGTTC 856  
QY 910 TTGCTACTCCAACTCGCGAAGAAATCCGGTGCATGAACCCAAACTACACAGACTTTCAGAT 969  
DB 857 TGGGAACCTCCAAAGGAGCAAAATCAGAGAAATGAACCCAAACTACACAGAAATTAAT 916  
QY 970 TCCCAAAATCAAAGCCCACTTGGCATAGGTTTTCACAGAGGATGCTCCGGAAG 1029  
DB 917 TCCCTCAAATTAAGGCACATCTTTGGACTTCTCCGACCCCGAATCTCCACCGGAGG 976  
QY 1030 CCATTGACCTTGCATCTCGGCTTCTTCAATACTACCAAGTCTAGCTTGCAGCTGCGCTCG 1089  
DB 977 CAATTGCACTGTGTAGCCGTCTGCTGGAGTATACACCAACTGCCGCACTAACCACTGG 1036  
QY 1090 AGGCATGTCGCATCCGTTTTTCAATGAAGTCCGTTGAGCCAAATGCTCGTCTTCCAAATG 1149  
DB 1037 AAGCTTGTGCATTCATTTTGTGATGAATTAAGGGACCCAAATGTCAAAACATCCAAATG 1096  
QY 1150 GCCGACCTCTACCAAGCTGTTCACACTTCA 1179  
DB 1097 GCGGAGACACACCTGCACCTTCAACTTCA 1126

## RESULT 12

US-08-602-264A-1  
; Sequence 1, Application US/08602364A  
; Patent No. 5837853  
; GENERAL INFORMATION:

; APPLICANT: Akihiko TAKASHIMA et al.  
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR  
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE  
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WENDEROTH, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.

QY	790	AGTATACATCATCCATTGATATATAGTCTGCTGGTTGTGTTCTGGCAGAGCTACTTCTTG	849
DB	1313	ATTATACCTCTAGTATAGATGTATGGTCTGCTGGCTGTGTGTTGGCTGAGCTGTACTAG	1372
QY	850	GCAGCGGTTATTTCGCCGGAGAAAATTCCTGTGACAGAGCTAGTGGAGATCATAAAGGTT	909
DB	1373	GACACCAATATTTCCAGGGGATAGTGGTGTGATCAGTTGGTAGAAATAATCAAGTCC	1432
QY	910	TTGGTACTCCAATCCGACGAGAAATCCGGTGCATGAACCCAACTACACAGACTTCAGAT	969
DB	1433	TGGGAATCCACAAGGGAGCAATCAGAGAAATGAACCCAACTACACAGAAATTTAAAT	1492
QY	970	TCCCAAAATCAAGGCCACCTCTGGGATAGAGTTTTCACAAAGCGATGCTCCCGAAG	1029
DB	1493	TCCTCAAAATTAAGGCACATCTCTTGGACTAAGGTCTTCGACCCCGAACTCCACCGAGG	1552
QY	1030	CNATTGACCTTGATCTCGGCTTCTTCAATACTCACCAAGTCTACGTTGCACTGCGCTCG	1089
DB	1553	CAATTGCACTGTGTAGCGTCTGTGAGTATACCAACTGCCCCGACTAACCACTGG	1612
QY	1090	AGGCATGTGGCATCCGTTTTTCAATGAATCCGTGAGCCAAATGCTCGTCTTCCAAATG	1149
DB	1613	AGCTTGTGCACATTCATTTTTTGATGAATACGGGACCAAAATGTCAAACCTACCAATG	1672
QY	1150	GCGAGCTCTACACCGTGTGTTCAACTTCA	1179
DB	1673	GCGGAGACACCTGCACCTTCAACTTCA	1702

RESULT 13  
 US-08-461-018A-1  
 ; Sequence 1, Application US/08461018A  
 ; Patent No. 6071694  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akiniko TAKASHIMA et al.  
 ; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: WENDEROOTH, LIND & PONACK  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; COUNTRY: D.C.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch,  
 ; MEDIUM TYPE: 1.44 mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/461,018A  
 ; FILING DATE: June 5, 1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/204,091  
 ; FILING DATE: March 2, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; REFERENCE/DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE:  
 ; TELEFAX:  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2088 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to genomic RNA  
 ; ORIGINAL SOURCE:

ORGANISM: human being  
US-08-461-018A-1

Query Match 24.1%; Score 394; DB 3; Length 2088;  
Best Local Similarity 65.5%; Pred. No. 1.9e-79;  
Matches 609; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 253 TTAGTTACATGCGCCGAACTGTTGTTGGAACAGGATCATTCGGAATTTGTTATTCAGGCAA 312  
DB 776 TCAGCTATACAGACACTAACTCATTTGGAATGGATCATTTGGTGTGTATATCAAGCCA 835

QY 313 AATGCTTGGAACTGGAGAATCAGTAGCCATTAAGAAGTTTTGCAAGATCCCGTTATA 372  
DB 836 AACTTTGTGATTCAGGAACTGGTCCGCAATCAAGAAAGTATTGCAAGCAAGAGATTTA 895

QY 373 AAAACCGAGAGTTGCAATTAATCGCACTAATGGACCATCCAAATGTTGGTTTCTTTCGAAAC 432  
DB 896 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGACTGACATAGTCCGATTCGGTT 955

QY 433 ATTGTTCTTCTC---TACAAGCTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGT 489  
DB 956 ATTCTTCTACTCCAGTGGTGAAGAAAGATGAGTCTATCTTAATCTGGTGTGGACT 1015

QY 490 ATGTACACAGACATTTGTCGGGTTTTGAAGCAGCTACTACTAGTTTCAACACCGGATGC 549  
DB 1016 ATGTTCCGAAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCC 1075

QY 550 CTAICTTCTATGTCAAACTTTACACATACCAAACTTTCAGAGGCTTGGCTTATATCCATA 609  
DB 1076 CTGTGATTTATGTCAAGTTGTATATGTATCATGCTGTTCCGAAGTTCGCTATATCCA-- 1133

QY 610 CTGCTCCTGCTGTCGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACA 669  
DB 1134 -TTCTTTTGGAACTGCCATCGGATATTAACCCGAGAACCTCTTTTGGATCCTGATA 1192

QY 670 CCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAGAACTACTGCTGAAAGTGAAACCA 729  
DB 1193 CTGCTGTATTAATACTCTGTGACTTTTGAAGTGCAGAGCAGTGTGCGAGGAGAACCA 1252

QY 730 ACATATCATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAG 789  
DB 1253 ATGTTTCTGATATCTGTTCTCGTACTATAGGACACAGAGTTGATCTTTGAGCCACTG 1312

QY 790 AGTATACATCATTCATATGATATATGCTGCTGCTGTTGTTCTGCGAGAGCTACTTCTTG 849  
DB 1313 ATTATACCTCTAGTATAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAG 1372

QY 850 GCGAGCGTTATTCGCGGAGAAATCTGTTGGAACAGCTAGTGGAGATCATAAAGGTTTC 909  
DB 1373 GACAAACCAATATTCGAGGGATGTTGTTGGATCAGTTGGTGAATAATCAAGGTTC 1432

QY 910 TTGGTACTCCAACTCGCGAAGAAATCCGCTGCATGAACCCAACTACACAGACTTTCAGAT 969  
DB 1433 TGGGAATCTCAACAGGAGGAAATCAGAGAATGAACCAAACTACACAGAAATTAAT 1492

QY 970 TCCCAAAATCAAGCCCACTTCGCAATAGGTTTTTCCAAAGCGGATGCTCCGGAAG 1029  
DB 1493 TCCCTCAAATTAAGCAATCTTCGACTTAAGGTTCTTCGACCCCGAACTCCACCGGAGG 1552

QY 1030 CCAATTGACCTTGATCTCGGCTTCTTCAATCTCAACCAAGTCTAGTTGCACTGCGCTCG 1089  
DB 1553 CAAATTGCACTGTTAGCGCTGCTGCTGGAGTATACACCAACTGCCCGGACTTAACCACTGG 1612

QY 1090 AGGCAATGCGCATCCGTTTTTCAATGAACCTCGGTGAGCAAAATGCTGCTTTCCAAATG 1149  
DB 1613 AGCTTTGCAATCAATTTTTTGAATGAATTAAGGAGCCCAAAATGTCAAACTACCAAAATG 1672

QY 1150 GCCGACCTCTACACCGTTGTTCAACTTCA 1179  
DB 1673 GCGGAGACACACCTGCACCTCTTCAACTTCA 1702

RESULT 14

US-09-216-958-1  
Sequence 1, Application US/09216958  
Patent No. 6248559  
GENERAL INFORMATION:  
APPLICANT: Akihiko TAKASHIMA et al.  
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST ALZHEIMER'S DISEASE (AS AMENDED)  
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WENDEROTH, LIND & PONACK  
CITY: Washington  
COUNTRY: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch,  
MEDIUM TYPE: 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/216,958  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/461,018  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE:  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2088 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to genomic RNA  
ORIGINAL SOURCE:  
ORGANISM: human being  
US-09-216-958-1

Query Match 24.1%; Score 394; DB 3; Length 2088;  
Best Local Similarity 65.5%; Pred. No. 1.9e-79;  
Matches 609; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 253 TTAGTTACATGCGCCGAACTGTTGTTGGAACAGGATCATTCGGAATTTGTTATTCAGGCAA 312  
DB 776 TCAGCTATACAGACACTAACTCATTTGGAATGGATCATTTGGTGTGTATATCAAGCCA 835

QY 313 AATGCTTGGAACTGGAGAATCAGTAGCCATTAAGAAGTTTTGCAAGATCCCGTTATA 372  
DB 836 AACTTTGTGATTCAGGAACTGGTCCGCAATCAAGAAAGTATTGCAAGCAAGAGATTTA 895

QY 373 AAAACCGAGAGTTGCAATTAATCGCACTAATGGACCATCCAAATGTTGGTTTCTTTCGAAAC 432  
DB 896 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTCCGATTCGGTT 955

QY 433 ATTGTTCTTCTC---TACAACGAGCTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGT 489  
DB 956 ATTCTTCTACTCCAGTGGTGAAGAAAGATGAGTCTATCTTAATCTGGTGTGGACT 1015

QY 490 ATGTACACAGACATTTGTCGGGTTTTGAAGCAGCTACTACTAGTTTCAACACCGGATGC 549  
DB 1016 ATGTTCCGAAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCC 1075

QY 550 CTAICTTCTATGTCAAACTTTACACATACCAAACTTTCAGAGGCTTGGCTTATATCCATA 609  
DB 1076 CTGTGATTTATGTCAAGTTGTATATGTATCATGCTGTTCCGAAGTTCGCTATATCCA-- 1133

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QY 610 CTGCTCTGCTGCTGCCAGAGATATAAAACCAACCAAAATCTTTTGGTTGATCCCA 669
Db 1134 -TTCCTTTGGAATCTGCCATCGGATATTAAACCGCAGAACTCTTGTGGATCCTGATA 1192

QY 670 CCCATCAGTGTAAAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGTGTAAAGGTGAACCAA 729
Db 1193 CTGCTGTATTAAACCTCTGTGACTTTTGGAAAGTCAAAAGCAGCTGTGTCCGAGGAGAACCA 1252

QY 730 ACATATCATATATCTCTCTCGGTATACCGAGCTCCAGAACTCATCTTTTGGTCCACAG 789
Db 1253 ATGTTTTCGTATATCTCTCTCGGTATACCGAGCTCCAGAACTCATCTTTTGGAGCCACTG 1312

QY 790 AGTATACATCATCTTGTATATATGCTCTGCTGTTGTTCTTGGCAGAGCTACTTCTTTG 849
Db 1313 ATTATACCTCTAGTATAGATGATGTTCTGCTGCTGTTGTTGGCTGAGCTGTACTAG 1372

QY 850 GGCAGCCGTTATTTCCGGGAGAAAATTTCTGTGACAGCTAGTGGAGATCATAAAGTTTC 909
Db 1373 GACAACTAATTTTCCAGGGGATAGTGTGTGGATCAGTTGGTAGAAAATAATCAAGGTCC 1432

QY 910 TTGGTACTCCAACTCCGGAAGAAATCCGGTGCATGTAACCCAACTACACAGACTTCAGAT 969
Db 1433 TGGGAATCTCCAAAGGAGCAAAATCAGAGAAATGAACCCAACTACACAGAAATTTAAAT 1492

QY 970 TCCCAAAATCAAAGCCCACTTGGCATAAGGTTTTTCCACAGCGGATGCCCTCCGGAAG 1029
Db 1493 TCCTCAAAATTAAGGCACATCTTGGACTTAAGTCTTCCGACCCCACTCCACCGGAG 1552

QY 1030 CCATTGACCTTGCATCTCGGCTTCTTCAATACACTACCAAGTCTAAGTTGCACCTCG 1089
Db 1553 CAATTGCACTGTGTAGCGCTCTGCTGGAGTATACACCAACTGCCCGCACTAACACCACTGG 1612

QY 1090 AGCATGTGGCATCCGTTTTCATGAAGTCTCGTGAGCAAAATGCTCTCTTCCAAATG 1149
Db 1613 AAGCTTGTGCACATTCATTTTGTGATGAATACGGGACCCAAATGTCAAACTACCAAAATG 1672

QY 1150 GCGGACCTCTACCACTGTTTCAACTTCA 1179
Db 1673 GCGGAGACACCTGCACTTCAACTTCA 1702

RESULT 15
US-08-602-264A-2
; Sequence 2, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

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; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; US-08-602-264A-2

Query Match 23.8%; Score 390; DB 2; Length 1972;
Best Local Similarity 64.2%; Pred. No. 1.5e-78;
Matches 620; Conservative 0; Mismatches 340; Indels 6; Gaps 2;

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QY 277 TTGGAAACAGGATCATTTCCGGAATTTGTTATCCAGGCAAAATGCTTGGAAAACCTGGAGAAATCAG 336
Db 324 TTGGAAATGGGTCTATTTGGTGTGTATATCAAGCCAACTTTGTGACTCAGGAGAACTGG 383

QY 337 TAGCCATTAAAGAGTTTTCGCAAGATCGCCGTTATAAAACCGAGAGTTGCAATTAATGC 396
Db 384 TGGCCATCAAGAAAGTTCTTCAGGACAGCGGATTTAAGAACCGAGAGCTCCAGATCATGA 443

QY 397 GACTAATGACACCATCCAATGTTGTTCTTGAAGCATTTGTTCTCTC---TACAAACA 453
Db 444 GAAAGCTAGTCACTGTGTAAACATAGTCCGATTCGGGTATTTCTTCTACTCGAGTGGCGAGA 503

QY 454 CTAGAGATGAGCTTCTCTCAATCTCGTTATGGAGTATGTACACAGAGACATTTGTACCGGG 513
Db 504 AGAAGATGAGGTCTACCTTTACCTGCTGCTGACTATGTTCCGGAACAGTGTACAGAG 563

QY 514 TTTTGAAGCACTATATAGTTCAAAACCGAGGATGCTATCTTTCTATGTCATAAATTTACA 573
Db 564 TCGCCAGACACTATATAGTCGAGCGCAAGCAGACACTCCCTGTGATCTATGTCAAGTTGTATA 623

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Db 681 ACATTAACCAACAGAACCTCTTGTGGATCTCTGATACAGCTGATTTAAACCTCTGCGACT 740

QY 694 TTGGAAAGTGCAAAAGTACTGTTGTAAGAGTGAAACCAACATATCATATATCTGCTCTCGGT 753
Db 741 TTGGAAAGTGCAAAAGTCTGTTCCGAGGAGAGCCCAATGTTTCATATATCTGTTCTCGGT 800

QY 754 ATTACCGAGCTCCAGAACTCATCTTTTGGTGGCAGAGTATACATCATCATTTGATATAT 813
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Db 921 GTGGTGTGGATCAGTTGGTGGAAATTAATAAAGTCTCTAGGAAACACCAACAAAGGAGCA 980

QY 934 TCCGTTGTCATGAAACCAACTACAGACTTCAGATTTCCACAAATCAAGAGCCACCTT 993
Db 981 TTAGAAATGAACCCCAAAATTTATACAGAAATTTCAATTTCCCAAAATCAAGGCAATCTCTT 1040

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QY 1114 ATGAATCGTGAGGCAAAATGCTCGTCTTCCAAATGGCGGACCTCTACCAACCGTTGTTC 1173
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Job time : 402.52 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 11285.4 Seconds  
(without alignment)  
6929.914 Million cell updates/sec

Title: X99696  
Perfect score: 1614  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1614	100.0	1614	8 ATASKIOTA	X99696 A.thaliana
2	1567	97.1	1572	8 AF019927	AF019927 Arabidops
3	1561.4	96.7	1582	8 AY035048	AY035048 Arabidops
4	1250.2	77.5	1255	8 AY051053	AY051053 Arabidops
5	972.2	60.2	1636	8 ATASKDZET	X94938 A.thaliana
6	962	59.6	1591	8 AY094423	AY094423 Arabidops
7	954.6	59.1	1566	8 AY064020	AY064020 Arabidops
8	951	58.9	1503	8 AY087542	AY087542 Arabidops
9	944.6	58.5	1270	8 AY096698	AY096698 Arabidops
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12	710.4	44.0	1636	8 AY086529	AY086529 Arabidops
13	708.8	43.9	1670	8 AY075699	AY075699 Arabidops
14	705.4	43.7	1863	8 AK102147	AK102147 Oryza sat
15	704	43.6	1738	8 ATASKRNA	X94939 A.thaliana
16	695.2	43.1	1744	8 BT009253	BT009253 Triticum
17	681.4	42.2	2055	8 AK073725	AK073725 Oryza sat
18	657.4	40.7	1825	8 AK100950	AK100950 Oryza sat
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24	581	36.0	2092	8 NTNSK6	Y08607 N.tabacum m
25	574	35.6	1249	8 AY142595	AY142595 Arabidops
26	574	35.6	1634	8 AF428327	AF428327 Arabidops
27	574	35.6	1667	8 AY046024	AY046024 Arabidops
28	573.8	35.6	1592	8 AB059621	AB059621 Oryza sat
29	573	35.5	1699	8 PPHSK6	X83620 P.hybrida m
30	572.2	35.5	2624	8 AK099742	AK099742 Oryza sat
31	571.4	35.4	1972	8 NTAJ4163	AJ224163 Nicotiana
32	570.6	35.4	1600	8 AK104687	AK104687 Oryza sat
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34	570.2	35.3	1859	8 AY339066	AY339066 Physcomit
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37	566	35.1	1496	8 ATASKA	X68525 A.thaliana
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42	561.4	34.8	2136	8 AK072390	AK072390 Oryza sat
43	560	34.7	1230	6 AY507663	AY507663 Sequence
44	560	34.7	1401	8 AY093347	AY093347 Arabidops
45	560	34.7	1630	8 AY062713	AY062713 Arabidops

## ALIGNMENTS

RESULT 1	ATASKIOTA	1614 bp	linear	PLN 13-FEB-1998
LOCUS	A.thaliana mRNA for shaggy-like kinase iota.			
DEFINITION	X99696			
ACCESSION	X99696.1 GI:1480077			
VERSION	AKS iota gene; shaggy-like kinase iota.			
KEYWORDS	Arabidopsis thaliana (thale cress)			
SOURCE	Arabidopsis thaliana			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE	1 Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.			
AUTHORS	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)			
JOURNAL	Plant Physiol. 113, 306-306 (1997)			
REFERENCE	2 (bases 1 to 1614)			
AUTHORS	Dornelas,M.C.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud (Parisxi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex, FRANCE			
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		/translation="MASLFGQPHALAPPLQHDGDALKRPELDSKEMSAVIEG NDAVYKRIISITIGGKNGPKQTSYMAERVVGTSGFIVFOAKLETGESVAIKKVL QDRYKNRLEQLQMPDHNPVLSLKHCFSTSRDELFLNLVMEYVETLYRVLRYHT SSNQRMPIFYVXLYTYQIFRGLAYIHTVPGVCHRDVKPONLLVDPLTHOVKLCDFGSA KVLVKEPNI SYICSRXYRPELIFGATEYITASIDIWSAGCVLAELLILGQPLFGENS VDQVLEIKVLGTPFREIRCMNPNTDFRFPQIKAHPHKVPFKRMPPEADILASRL LQISPLRCITALEACAHFPFNELRPNARLPNGRPPLFNFQELGGHSMELINRLI PEHVRQMSLTGLQNS"			
ORIGIN		Query Match 100.0%; Score 1614; DB 8; Length 1614;			
		Best Local Similarity 100.0%; Pred. No. 0;			
		Matches 1614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AAGCAAGAGAGAGAGAAAATTAGACTTTTACTCATTTGTTCAAGTGGTTGAGAGAGAAAAGA	60		
DB	1	AAGCAAGAGAGAGAGAAAATTAGACTTTTACTCATTTGTTCAAGTGGTTGAGAGAGAAAAGA	60		
QY	61	GTAAGAAAGCAGATGCGCTCATTTACATTTGGGCGCTCAGCCTCATGCTCTTGTCTCGCGG	120		
DB	61	GTAAGAAAGCAGATGCGCTCATTTACCATTTGGGCGCTCAGCCTCATGCTCTTGTCTCGCGG	120		
QY	121	CTGCAGCTTCACGACGGCGACGCTTTGAAACGGCGTCTCTGAATTGGATTCTGATAGGAA	180		
DB	121	CTGCAGCTTCACGACGGCGACGCTTTGAAACGGCGTCTCTGAATTGGATTCTGATAGGAA	180		
QY	181	ATGTCTGCAGCTGTTATTGAGGGAATGACGTGTTTACTTGTCATATCATTTCCACTACT	240		
DB	181	ATGTCTGCAGCTGTTATTGAGGGAATGACGTGTTTACTTGTCATATCATTTCCACTACT	240		
QY	241	ATAGGAGGCAAAAACGGCGAACCAAGACGACCAATTAGTTACTATGCTGAGCGGGTGT	300		
DB	241	ATAGGAGGCAAAAACGGCGAACCAAGACGACCAATTAGTTACTATGCTGAGCGGGTGT	300		
QY	301	GGAAACAGGTTTCATTCGGGATGTTTTCAGGCGAAATGCTTGGAACCTGGAGAACTCAGTA	360		
DB	301	GGAAACAGGTTTCATTCGGGATGTTTTCAGGCGAAATGCTTGGAACCTGGAGAACTCAGTA	360		
QY	361	GCCATTTAAAAGGCTTTGCAAGATCGACGCTATAAAAAACCGTGAGTTGCAACTAATGCGA	420		
DB	361	GCCATTTAAAAGGCTTTGCAAGATCGACGCTATAAAAAACCGTGAGTTGCAACTAATGCGA	420		
QY	421	CGAATGGATCACCAGATGTCATCTCTTGAAGCAGCTGTTCTTCTCTACAACGAGTAGA	480		
DB	421	CCAATGGATCACCAGATGTCATCTCTTGAAGCAGCTGTTCTTCTCTACAACGAGTAGA	480		
QY	481	GATGAGCTCTTCTCAACCTGTTGATGGAGTATGTACCTGAGACTTTATACCGGGTTTG	540		
DB	481	GATGAGCTCTTCTCAACCTGTTGATGGAGTATGTACCTGAGACTTTATACCGGGTTTG	540		
QY	541	AGGCATATATAGTTCTAATCAGAGATGCCAAATTTTCTATGTCAGCTTTACACATAT	600		
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QY	661	AAACCAAAAATCTCTTGGTTGATCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGA	720		
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QY	841	GCTGGTGTGTACTGCGCAGAGCTTCTTCTTGCCAGCCGCTTATTTCCAGAGAGAAATTC	900		
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QY	901	GTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGTTACTCTCAACTCGTGAAGAAATTC	960		
DB	901	GTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGTTACTCTCAACTCGTGAAGAAATTC	960		
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DB	1021	AAAGGTTTTTATAAAGCGATGCTCCAGAGCAATAGAGCTTGCATCTCGGCTTCTTCAA	1080		
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DB	1081	TATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTCTCATCCGTTTTTCAATGAA	1140		
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DB	1141	CTCCGAGAGCCAAACGCCGCTCTCCAAATGCTGCTCAATTACCGCCATTTGTTCAATTT	1200		
QY	1201	AAACAAGAGTTAGTGGAGCTTCAATGGAGCTAAATCAACAGGCTAATACCTGAGCATGT	1260		
DB	1201	AAACAAGAGTTAGTGGAGCTTCAATGGAGCTAAATCAACAGGCTAATACCTGAGCATGT	1260		
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QY	1321	GAGGAGAAAGCAGGTTTACTACTTTTATTCATAGTTGACAGGTTCAACAGTATATTA	1380		
DB	1321	GAGGAGAAAGCAGGTTTACTACTTTTATTCATAGTTGACAGGTTCAACAGTATATTA	1380		
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DB	1381	CCACGACTATTATCAGCTTCTATACCGTAGTAAAGTCAATTCAGCTTTTGGAGAAATC	1440		
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DB	1441	AGATGCTGATAATGCGTCTATTTTATTTTATCTTACCTTGAGCTGAGAGTGGAGAGAC	1500		
QY	1501	ACTGTTCTCTCGGTATTTTGTATATGTTTGTCTGTAATAAATTTCTGACAGATACGT	1560		
DB	1501	ACTGTTCTCTCGGTATTTTGTATATGTTTGTCTGTAATAAATTTCTGACAGATACGT	1560		
QY	1561	AGAGACAAAAGAAAAACGAGGTGATAATATTAACCAAAAAAATAAAAAA 1614			
DB	1561	AGAGACAAAAGAAAAACGAGGTGATAATATTAACCAAAAAAATAAAAAA 1614			

RESULT 2  
AF019927  
LOCUS  
DEFINITION Arabidopsis thaliana GSK3/shaggy-like protein kinase (GSK1) mRNA,  
complete cds.  
ACCESSION AF019927  
VERSION AF019927.1 GI:2444276  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1 (bases 1 to 1572)  
AUTHORS Piao,H.L., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B., Kim,S.H. and  
Hwang,I.  
TITLE An Arabidopsis GSK3/shaggy-like gene that complements yeast salt  
stress-sensitive mutants is induced by NaCl and abscisic acid  
JOURNAL Plant Physiol. 119 (4), 1527-1534 (1999)  
MEDLINE 99214484



PUBMED 10198112  
REFERENCE 2 (bases 1 to 1572)  
AUTHORS Piao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B. and Hwang,I.  
TITLE Direct Submission  
JOURNAL Submitted (18-AUG-1997) Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Chinju 660-701, Korea  
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## RESULT 4

AY051053

LOCUS

DEFINITION

AY051053

ACCESSION

VERSION

KEYWORDS

SOURCE

1255 bp mRNA linear PLN 18-SEP-2002  
 Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA,  
 complete cds.  
 AY051053  
 AY051053.1 GI:15293238  
 Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
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## REFERENCE

AUTHORS

1 (bases 1 to 1255)  
 Yanada,K., Liu,S.X., Sakano,H., Pham,P.K., Banno,J., Egu,P.,  
 Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,  
 Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,  
 Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and  
 Theologis,A.

## TITLE

JOURNAL

REFERENCE

AUTHORS

Arabidopsis Open Reading Frame (ORF) Clones  
 Unpublished  
 2 (bases 1 to 1255)  
 Yanada,K., Liu,S.X., Pham,P.K., Banno,J., Banno,P., Dale,J.M.,  
 Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.I.,  
 Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,  
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,  
 Jones,T., Kaniya,A., Karlin-Neumann,G., Kawai,J., Kim,C.,  
 Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Narusaka,M.,  
 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,  
 Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and  
 Theologis,A.

## TITLE

JOURNAL

COMMENT

Direct Submission  
 Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan  
 Street, Albany, CA 94710, USA  
 The RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kaniya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and  
 sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yanada,K.,  
 Liu,S.X., Pham,P.K., Banno,J., Banno,P., Dale,J.M., Goldsmith,A.D.,  
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.I., Tang,C.C.,  
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,  
 Cheuk,R., Jones,P., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B.,  
 Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,  
 Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yanada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally  
 to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP  
 /PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis  
 genome submitted to GenBank.

## FEATURES

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1612

1582

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 REFERENCE  
 1 Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.  
 TITLE  
 Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PCR97-008)  
 JOURNAL  
 Plant Physiol. 113, 306-306 (1997)  
 REFERENCE  
 2 (bases 1 to 1636)  
 AUTHORS  
 Dornelas, M.C.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSA Cedex, FRANCE  
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DB	249	ACCATTAGTTACATGGCGCAACGGTGTGTTGAAACAGGATCATTCGGAATTTGATTTCCAG 308	
QY	331	GGGAATGCTTGGAACTGGGAATCAGTAGCCATTAAGAGGTTTTCGCAAGATCGACGC 390	
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QY	391	TATAAAACCGTGAGTTGCAATTAATGCGACCAATGGATCACCAATGTCTATCTCTTG 450	
DB	369	TATAAAACCGGAGAGTTGCAATTAATGCGACTAATGGACCATCCAAATGTGTTTCTTG 428	
QY	451	AAGCACTGTTCTTCTTCAACAGAGTAGAGTCTCTCTCAACCTCTTTATGGAG 510	
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QY	871	GGCGAGCGGTTATTTCCAGGAGAAATTCAGTTGATTCAGTGTGGAGATCATATAAGGTT 930	
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QY	1231	CTAATCAACAGCTAATACCTGAGCATGTGAGCACCAAAATGAGCACAGGATTACAAAAC 1290	
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QY	1291	AGTTAAAAAC-----TGTGCAATGCTGAAAGAGAAAGAGAGAGAAAG 1331	
DB	1269	CAAGCTGGACCTAGAAAGCGATCTCGAGATGCTTTTCCAGAGCAAAATGCGGCTTAT 1328	
QY	1332	CAGGTTTACTACTTTTATTTGATAGTTGACAGGTTCAACAGTATATTAAACCAAGCTATT 1391	
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QY	1452	ATTGCGTCTATTTTCTTCTTAGCTTGGAGAGTGGAGAGACACATGTTTCTCTCG 1511	
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DEFINITION	Arabidopsis thaliana At2g30980/F7P1.19 mRNA, complete cds.				
ACCESSION	AY094423				
VERSION	AY094423.1 GI:20453107				
KEYWORDS	FLI CDNA.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1 (bases 1 to 1591)				
AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C., Palm, C.J., Quach, H.L., Sakurai, T., Saou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yanada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.				
TITLE	Arabidopsis cDNA clones				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1591)				
AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,				

TITLE JOURNAL	Kawai, J., Lam, B., Lee, J.M., Lin, J., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinzaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.	
	Direct Submission Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA	
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.	
	The Salk, Stanford, PEGC (SSP) Consortium members carried out the sequencing and annotation of the RAPL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.	
FEATURES	Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.	
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 REFERENCE 1 (bases 1 to 1503)  
 AUTHORS Haas,B.J., Volkovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,  
 Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.  
 TITLE Full-length messenger RNA sequences greatly improve genome  
 annotation  
 JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)  
 MEDLINE 22088475  
 PUBMED 12093376  
 REFERENCE 2 (bases 1 to 1503)  
 AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
 Feldmann,K.  
 TITLE Full-length cDNA from Arabidopsis thaliana  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 1503)  
 AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and  
 Feldmann,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,  
 Malibu, CA 90265, USA  
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made  
 available to TIGR and Genbank. The following quality assessment of  
 this set was done by comparison with known proteins: two percent of  
 the clones are estimated to be 5'-truncated; less than one percent  
 are 3'-truncated; approximately two percent represent alternative  
 splice variants, including unspliced introns and spliced exons; one  
 percent may contain premature stop codons; five percent may have  
 frame shifts in a coding region. A sequence is considered to be  
 5'-truncated if it lacks the translation initiation start (ATG). A  
 sequence is considered to be 3'-truncated if it lacks the  
 C-terminal end of the encoded protein. Please note that these cDNA  
 sequences are derived from the Ws or Laer ecotypes and therefore  
 may contain polymorphisms when compared to sequences from Col-0.  
 Genet carried out the library production and sequencing of the  
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 QY 511 TATGTACCTGAGACTTTATACCGGTTTGGAGCACTATAGTTCTTAATCAGAGGATG 570  
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 Db 1158 GCGCGACCTCTACCCACCGTGTTCATTTCAAAAGAGTTAGGTAGGCTTCAATGGAG 1217  
 QY 1231 CTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAGCAGATTACAA 1287  
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RESULT 9  
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 LOCUS Arabidopsis thaliana putative shaggy protein kinase dzeta  
 DEFINITION (A2930980) mRNA, complete cds.  
 ACCESSION AY096698  
 VERSION AY096698.1 GI:20465726  
 KEYWORDS FLI CDNA.  
 SOURCE Arabidopsis thaliana (chale cress)  
 ORGNISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE 1 (bases 1 to 1270)  
 AUTHORS Yanada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,  
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,  
 Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,  
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,  
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,  
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,  
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,  
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Arabidopsis Open Reading Frame (ORF) Clones  
 Unpublished  
 JOURNAL 2 (bases 1 to 1270)  
 REFERENCE Yanada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,  
 Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,  
 Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,  
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,  
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,  
 Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,  
 Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,  
 Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Direct Submission  
 JOURNAL Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan  
 Street, Albany, CA 94710, USA  
 COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN  
 Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
 Hayashizaki, Y. and Shinozaki, K.  
 The Salk, Stanford, PGE (SSP) Consortium members constructed and  
 sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yanada, K.,  
 Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,  
 Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,  
 Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,  
 Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B.,  
 Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,  
 Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.  
 Yanada, K. (SSP/PGE) and Seki, M. (RIKEN GSC) contributed equally  
 to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP  
 /PGE) contributed equally to this work as PI.

Annotation is based on the January 2002 version of the Arabidopsis  
 genome submitted to GenBank.  
 FEATURES  
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Db 242 AACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTGTGTGAAGCAATGCTTCT 301

Qy 464 TCTCTACACGAGTAGAGTAGCTTCTCTCAACCTTGTATGGAGTAGTACCTGAGA 523

Db 302 TTTTCGACTACAGTAAGAGAGAGCTTCTTGAACCTTGTGTATGGAGTAGTCCCTGAGA 361

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Db 662 CTATGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721

Qy 884 TTCCAGGAGAAATTCAGT 943

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RESULT 11  
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LOCUS AX506180 1143 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 875 from Patent W00216655.  
ACCESSION AX506180  
VERSION AX506180.1 GI:23387417

KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.  
AUTHORS Stress-regulated genes of plants, transgenic plants containing same, and methods of use  
TITLE Patent: WO 0216655-A 875 28-FEB-2002;  
JOURNAL The Scripps Research Institute (US); Syngenta Participations AG (CH)

FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Query Match 44.0%; Score 710.4; DB 6; Length 1143;  
Best Local Similarity 77.1%; Pred. No. 2.6e-166;  
Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

Qy 164 TGGATTCGATAAGAAATGCTGCAGCTGTATTGAGGAAATGACGCTGTACTGTGTC 223

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Qy 224 ATATCATTTCCACTACTATAGAGGCAAAAGCGGCAACCAAGCAAGCAACATTAGTTACA 283

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Qy 344 AAACCTGGAGATCAGTAGGCATTAAGAGCTTTCAGAGATCGAGCTATATAAAACCGTG 403

Db 182 AGACTGGAGAAACCGTGGCGATTAAGAGAGTGTTCAGAGATGAAGATACAAAGAACCGAG 241

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Db 242 AACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTGTGTGAAGCAATGCTTCT 301

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Qy 524 CTTTATACCGGTTTGGAGCACTATATAGTTCATATCAGAGATGCAATTTCTATG 583

Db 362 GCTTGTATCGAGTCTCTGAACATATATAGTAGTGAACCAACCAAGAAATGCTCTGTCTATG 421

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Db 662 CTATGTATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721

Qy 884 TTCCAGGAGAAATTCAGT 943

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QY      1064  CATCTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCAGCTCGGCTCGAAGCATGTGCTC 1123
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QY      1124  ATCCGTTTTCATGAATCCGAGAGCCAAACGCCGCTCTTCAATGTGCTGCATTAAC 1183
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QY      1244  TAATACCTGAGCATGTGAGACGACCAATGAGCACAGGATT 1283
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## RESULT 12

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LOCUS      AY086529      1636 bp      mRNA      linear      PLN 14-APR-2003
DEFINITION Arabidopsis thaliana clone 256076 mRNA, complete sequence.
ACCESSION  AY086529
VERSION    AY086529.1  GI:21405239
KEYWORDS  FLI CDNA.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE  1 (bases 1 to 1636)
           Haas, B.J., Volfevsky, N., Town, C.D., Troukhan, M., Alexandrov, N.,
           Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
           Full-length messenger RNA sequences greatly improve genome
           annotation
           Genome Biol. 3 (6), RESEARCH0029 (2002)
PUBMED    12093376
REFERENCE  2 (bases 1 to 1636)
           Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
           Feldmann, K.
           Full-length cDNA from Arabidopsis thaliana
           Unpublished
REFERENCE  3 (bases 1 to 1636)
           Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and
           Feldmann, K.
           Direct Submission
           Submitted (11-MAR-2002) Ceres, Inc., 3007 Malibu Canyon Road,
           Malibu, CA 90265, USA
COMMENT   This clone sequence is one of 5,000 Ceres full-length cDNAs made
           available to TIGR and Genbank. The following quality assessment of
           this set was done by comparison with known proteins; two percent of
           the clones are estimated to be 5'-truncated; less than one percent
           are 3'-truncated; approximately two percent represent alternative
           splice variants, including unsplined introns and spliced exons; one
           percent may contain premature stop codons; five percent may have
           frame shifts in a coding region. A sequence is considered to be
           5'-truncated if it lacks the translation initiation start (ATG). A
           sequence is considered to be 3'-truncated if it lacks the
           C-terminal end of the encoded protein. Please note that these cDNA
           sequences are derived from the Ws or Laer ecotypes and therefore
           may contain polymorphisms when compared to sequences from Col-0.
           Genset carried out the library production and sequencing of the

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full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.

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## ORIGIN

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Query Match      44.0%; Score 710.4; DB 8; Length 1636;
Best Local Similarity 77.1%; Pred. No. 2.5e-166;
Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

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QY      224  ATATCATTTCCACTACTATAGGAGGCAAAACCGCGAACCAAGAGCAGACCATTAGTTACA 283
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Db      294  TGGCGGAGCGAGTTGTTGGTACAGGCTCTTCGGGATCGTTTTTCCAAAGCAAAATGTTGG 353
QY      344  AAACCTGGGAATCAGTAGCCATTAAAGAGTCTTCAAGATCGAGCTATAAAACCGTG 403
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QY      404  AGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCATCTCTTGAAGCACTGTTTCT 463
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QY      524  CTTTATACCGGTTTGGGCACTATACCTAGTTCTTAATCAGAGGATGCCAAATTTCTATG 583
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RESULT 13

AY075699

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AY075699

Arabidopsis thaliana AT4g18710/P28A21\_120 mRNA, complete cds.

1670 bp mRNA linear PLN 18-FEB-2002

AY075699.1

GI:18700187

FLI CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 1670)

Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayaehizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Arabidopsis cDNA clones

Unpublished

2 (bases 1 to 1670)

Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayaehizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Direct Submission

Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayaehizaki, Y. and Shinozaki, K.

The Salk, Stanford, PEEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

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## RESULT 14

AKI02147  
LOCUS  
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ACCESSION AKI02147

VERSION AKI02147.1 GI:32987356

KEYWORDS FLI CDNA; CAP trapper.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of  
Agrobiological Sciences Rice Full-Length cDNA Project Team,  
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,  
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,  
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,  
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International  
Science Genome Sequencing & Analysis Group: Ohtsuki,K.,  
Tada,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,  
Kuroaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,  
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Miura,J.,  
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,  
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,  
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,

## TITLE

## JOURNAL

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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# SUMMARIES

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16	665.8	41.3	1789	3 AAC51694	Aac51694 Zea mays
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32	534	33.1	1523	8 ACC57974	Acc57974 Soybean p
33	532.8	33.0	1866	8 AAL55586	Aal55586 cDNA enco
34	532.6	33.0	1344	3 AAC42818	Aac42818 Arabidops
35	523.4	32.4	1429	5 AAH47003	Aah47003 Soy bean
36	523.4	32.4	1429	6 ABQ82533	Abq82533 Soybean g
37	516.8	32.0	1757	8 ACC57969	Acc57969 Canola pr
38	503	31.2	1654	8 ACC57971	Acc57971 Canola pr
39	496.8	30.8	1296	6 ABZ12869	Abz12869 Arabidops
40	496.8	30.8	1296	6 ADG87959	Adg87959 A. thalia
41	496.8	30.8	1296	12 ADN73136	Adn73136 Thale cre
42	400	24.8	1100	8 ACC57961	Acc57961 Protein k
43	397.4	24.6	608	13 ACN53505	Acn53505 Cotton an
44	385.2	23.9	1230	10 ADK66952	Adk66952 Gene #42
45	385.2	23.9	1389	4 AAD11491	Aad11491 Human gly

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KW	protein identification; signal transduction pathway; metabolic pathway;				
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Query Match 58.9%; Score 951; DB 3; Length 1503;			
Best Local Similarity 85.9%; Pred. No. 1.9e-246;			
Matches 1080; Conservative 0; Mismatches 170; Indels 7; Gaps 2;			
QY	38	TTCACTGGTTGAGAGAGAAAGAG-TAAAAAGCAGATGGCTCATTTACCATTTGGGGCT 96	
DB	18	TTCACTGGAGAGAGAAAGTTAGAGTTGTAAGAGCAGATGCTTCGATACCATTTGGGGCT 77	
QY	97	CAGCCTCATGC-----TCTTCTCCGCGCTGACGTTTACGAGCGGAGCGCTTTTGAAA 150	
DB	78	CCTCAGCCTCCGCTCTTTAGCTCTCAGCCGCGCATCTTCAGCGCGAGATTCTTTTGAAA 137	
QY	151	CGCCGCTCTGAAATGGATTCTGATAAGGAAATGCTGACAGCTGTTTATTGAGGGAAATGAC 210	
DB	138	CGTGTCCCGATATAGACAAACGACAGGAAATGTCTGCTGCTGTTATAGAGGAATGAT 197	
QY	211	GCTGTTACTGTCATATCATTTTCCACTACTATAGAGGCAAAACGGCGAACCAAGCAG 270	
DB	198	GCTGTTACCGGTACATAATTTCTACTCAATTTGGAGGCAAAATGCGTGAACCTAAACAG 257	
QY	271	ACCATTTAGTTACATCGCTGAGCGGTGTTGGAACAGAGTTTCAATTCGGGATTTTTCAG 330	
DB	258	ACCATTTAGTTACATGGCGGAACGTGTTGTTGGAACAGAGTCAATTCGGAATTTGATTCAG 317	
QY	331	CGAAATGCTTGGAAATCGGAGAAATCAGTAGCCATTAAAAAGGTCTTCAAGATCGAGCG 390	
DB	318	GCATAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAAGAGTTTTCAGAGATCGCGT 377	
QY	391	TATAAAACCGGTAGTTGCAACTAATGGACCAATGGATACCCAAATGTCATCTCCTTG 450	
DB	378	TATAAAACCGGAGAGTTGCAATTAATGGACCTAATGGACCATCCAAATGTGTTTCTCTG 437	
QY	451	ANGCACTGTTTCTTCTACACGAGTAGAGATGAGCTTCTTCTCAACCTGTTATGAG 510	
DB	438	AAGCATTGTTTCTTCTTCTACACGAGTAGAGATGAGCTTCTTCTCAATCTGTTATGAG 497	

QY	511	TATGTACTGAGACTTTATACCGGGTTTGGAGCACTATACTAGTTCTTAATCAGAGGATG 570	
DB	498	TATGTACCAGAGACATTGTACCGGGTTTGAAGCACTATACTAGTTCAAAACAGCGGATG 557	
QY	571	CCAAATTTCTATGTCAAGCTTTTACACATATCAAAATCTTTAGAGGTTTGGCTTTACATCCAT 630	
DB	558	CCTATCTTCTATGTCAAACTTTTACATACCAATCTTTCAGAGGCTTGGCTTTATATCAT 617	
QY	631	ACTGTTCCCGGTGTTGCCACAGAGATGTGAACCAACAAAATCTCTTGGTTGATCCCTTG 690	
DB	618	ACTGCTCTGCTGCTGCCACAGAGATGTGAACCAACAAAATCTTTGTTGATCCCTTC 677	
QY	691	ACCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGCMAAAGTATTTGGTCAAGGTTGAACCA 750	
DB	678	ACCATCAGTGAAGCTCTGTGATTTTGGAAAGTGCMAAAGTATTTGGTCAAGGTTGAACCA 737	
QY	751	AACATATCATATCTGCTCCCGTTTATTATCGTGTCTCAGAACTCATCTTTGGCGCCACA 810	
DB	738	AACATATCATATCTGCTCTCGGTATTTCCGATCTCCAGAACTCATCTTTGGTGGCCACA 797	
QY	811	GAGTATACAGCATCCATAGATATATGCTCTGCTGTGTGTGATCTGGCAGAGCTTCTTCTT 870	
DB	798	GAGTATACATCATCATTTGATATGCTCTGCTGTGTGTGATCTGGCAGAGCTTCTTCTT 857	
QY	871	GGCAGCGGTTATTTCCAGGAGAAAATTTCACTGTTGATCAGCTTGTGGAGATCATAAAGTT 930	
DB	858	GGCAGCGGTTATTTCCCGGAGAAAATTTCTGTGGACCGGCTAGTGGAGATCATAAAGTT 917	
QY	931	CTTGTACTCCAAGCTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGG 990	
DB	918	CTTGTACTCCAAGCTCGGGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAG 977	
QY	991	TTCCCAAAATCAAAGCTCACCTTTGGCAAGGTTTTTTCATAAACGGATGCTCCAGAA 1050	
DB	978	TTCCCAAAATCAAAGCTCACCTTTGGCAAGGTTTTTTCATAAACGGATGCTCCAGAA 1037	
QY	1051	GCAATAGACCTTGATCTCGGCTTCTTCAATTTCCAAAGTCTACGCTGACCTGGCTC 1110	
DB	1038	GCAATAGACCTTGATCTCGGCTTCTTCAATTTCCAAAGTCTACGCTGACCTGGCTC 1097	
QY	1111	GAAAGTGTGCTCATCTCGGTTTTTCAATGAACCTCCGAGAGCCAAAGCCGCTTCCAAAT 1170	
DB	1098	GAGGATGTGGCATTCGCTGTTTTTCAATGAACCTCCGAGAGCCAAAGTCTGCTTCCAAAT 1157	
QY	1171	GCTGCTCATTTACCGCCATTGTTCAATTTCAAAAGAGTTAGGTGGAGCTTCAATGGAG 1230	
DB	1158	GGCGGACCTTACCACCGTGTCTTCAATTTCAAAAGAGTTAGGTGGAGCTTCAATGGAG 1217	
QY	1231	CTAATCAACAGGCTTAATACCTGAGCATGTGAGACGCAAAATGAGCAGCAGGATTAACA 1287	
DB	1218	CTTATCAACAGGCTTAATACAGAGCATGTGAGGCGCAGATGAATGGTGGCTTTTCCA 1274	

RESULT 4  
 ACC57975  
 ID ACC57975 standard; cDNA; 1744 BP.  
 XX  
 AC ACC57975;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Soybean protein kinase stress-related polypeptide Gmpk-3 cDNA.  
 XX  
 KW Gmpk-3; protein kinase stress-related polypeptide; PKSRP; enzyme;  
 KW transgenic plant; plant; stress tolerance; drought tolerance;  
 KW salt tolerance; cold tolerance; soybean; gene; ss.  
 OS Glycine max.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 40..1302  
 FT /\*tag= a

FT	WT02003040171-A2.	/product= "GmpK-3"	
PN	15-MAY-2003.		
XX	12-NOV-2002; 2002WO-US036374.		
PD	09-NOV-2001; 2001US-0346096P.		
XX	(BADI ) BASF PLANT SCI GMBH.		
PR	Van Thielens N, Da Costa E SilvaO, Chen R;		
XX	WPI: 2003-441522/41.		
XX	P-PSDB; ABR42368.		
XX	New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type variety of the plant.		
PT	Claim 1; Page 96-97; 111pp; English.		
PS	The present sequence is a full-length cDNA encoding GmpK-3, a novel soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was identified on the basis of homology to Physcomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. GmpK-3 is an example of PKSRPs of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low temperature		
XX	Sequence 1744 BP; 502 A; 379 C; 380 G; 483 T; 0 U; 0 Other;		
XX	Query Match	47.3%; Score 763.2; DB 8; Length 1744;	
XX	Best Local Similarity	78.6%; Pred. No. 1.3e-195;	
XX	Matches 912; Conservative	0; Mismatches 248; Indels 0; Gaps 0;	
QY	115	CCGCGCTGCGAGTTCACGACGCGCGAGCTTTGAAACGCGCTCTGAAATGGATTCGAT	174
DB	112	CCGCGCGAGTCTCAGCGCGAACCCGAAGTTCTCTCGCGGAGTCCGATGTGGAGACCGAT	171
QY	175	AAGGAATGCTCGACGTGTTATGGAGGAATGAGCTGTACTGCTCATATCATTTCC	234
DB	172	AAGGATATGTCAGCTACTGTCTATGGAGGAATGATGCTGCTACCTGGCCACATAATCTCC	231
QY	235	ACTACTATAGGAGGCAAAACCGCGAACCAAGCAGACCATTAAGTTACATGGCTGAGCGG	294
DB	232	ACCACAATTTGGAGGCAAAATGGGAACTTAAGAGNCCATCAGTTACATGGCAGAACGT	291
QY	295	GTTGTTGGAAACAGGTCATTCGGGATGTTGTTTTCAGCGGAAATGCTTGGAAATCGAGAA	354
DB	292	GTTGTTGGCACTGGATCAATTTGGAGTGTGTTTTCAGGCAAGTGTGAGACTGGAGAA	351
QY	355	TCAGTAGCCATTAAGAGGCTTTCAGAGTCGAGCTATTAAGACCGTGGATGCAACTA	414
DB	352	GCAGTGGCTATTAAGAGGCTTTCAGAGTCGAGCTATTAAGACCGTGGATGCAACTA	411
QY	415	ATCGGACCAATGGATCACCAGGATGTCATCTCTGAGGACATGTTCTCTCTACAACG	474
DB	412	ATCGGCTTAATGGATCACCAGGATGTCATCTCTGAGGACATGTTCTCTCTACAACA	471
QY	475	AGTAGAGATGAGCTCTTCTCCAACTTTATGGAGATGATGATCCTGAGACTTTATACCGG	534
DB	472	AGCAGAGATGAATCTTTTCTAAACTTGGTAATGGAATATGTTCCCGAATCAATGTACCGA	531
QY	535	GTTTGTGAGGCACTATAGTCTTAATCAGAGATGCCAATTTCTATGTCAGCTTTAC	594
DB	532	GTTATAAGCACTACACTACTATGATGACCAAGAGATGCCCTCTCATCTATGTGAACGTGAT	591
QY	595	ACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTCCACAGAG	654
DB	592	ACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTCCACAGAG	651
QY	655	GATGTGAACCAACAAATCTCTTGGTTGATCCCTTGAACCCATCAGGTTAAGCTGTGTGAT	714
DB	652	GATGTGAAGCCCTCAAAATCTTTTGGTTTCACTCTCTTACTCACCAGTTAAGCTATGTGAT	711
QY	715	TTTGGAGTGCAGAAAGTATTGGTCAAGGTGAACCAACATATCATATATCTGCTCCCGT	774
DB	712	TTTGGAGTGCAGAAAGTATTGGTCAAGGTGAATCAACATTTCAATATATGTTCCAGCT	771
QY	775	TATTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATA	834
DB	772	TACTATCGGCTCCAGAACTAATATTGGTGCAACAGAAATACACAGCTTCTTATGATATC	831
QY	835	TGGTCTGCTGTTGTTGTTACTGGCAGAGCTTCTTTTGGCAGCGGTTATTTCCAGAGAA	894
DB	832	TGGTCAAGCTGTTGTTGTTTCTTCTGAACTTCTTTAGGACAGCCATTAATTTCTCGAGAA	891
QY	895	AATTCAAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGTGTTACTCCAACTCGTGAAGAA	954
DB	892	AACCAAGTGGACCAACTTGTGGAATTAATCAAGGTTCTTGGTACTCCAAACAGCGAGGAA	951
QY	955	ATTGATGTATGAACCCGAACTACAGAGTTTATGTTTCCCAAAATCAAAAGCTCACCT	1014
DB	952	ATCCGTTGTTATGAACCCAAATTTATACAGAGTTTATGATTCCTCAGATTAAAGCTCATCT	1011
QY	1015	TGGCAAGAGTTTTCATTAACGGATGCTTCAGAGCAATAGACCTTGCATCTCGGCTT	1074
DB	1012	TGGCAAGAGTTTTCATTAACGGATGCTTCAGAGCAATAGACCTTGCATCTCGGCTT	1071
QY	1075	CTTCAATATTCACCAAGTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1134
DB	1072	CTTCAATATTCACCAAGTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1131
QY	1135	AATGAATCTCCGAGAGCCAAACCGCTCTTCCAAATGCTGCTCAATACCGGCAATGTTTC	1194
DB	1132	GATGAGCTTCGCGAACCAATGCGCGGTACCTAATGGCGCTCCACTGCCCCACCTTTTC	1191
QY	1195	AATTTCAACAGAGTTAGGTGAGCTTCAATGGAGCTTAATCAACAGGCTAATACCTGAG	1254
DB	1192	AATTTCAACAGAGTTAGGTGAGCTTCAATGGAGCTTCAATGGAGCTTCAATGGAGCT	1251
QY	1255	CATGTGAGACGCAAAATGAG	1274
DB	1252	CATATTAGCGCGAGATGGG	1271
RESULT 5	AAC47997		
ID	AAC47997 standard; DNA; 1657 BP.		
XX	AAC47997;		
AC	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.		
DE	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
XX	Arabidopsis thaliana.		
XX	EP1033405-A2.		
PN	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-00301439.		
PF	25-FEB-1999; 99US-0121825P.		
XX	05-MAR-1999; 99US-0123180P.		
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PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157533P.





CC	biomass, enhanced survival capacity, stress tolerance, plant architecture
CC	or physiology, altered endoreduplication, biochemistry, signal
CC	transduction, storage lipid mobilisation and/or altered photosynthesis,
CC	each relative to the corresponding wild type plants. Accordingly, these
CC	sequences can also be useful as positive or negative selectable markers
CC	during transformation of cells or tissues. The identified genes play a
CC	role in a variety of biological processes such as DNA replication, cell
CC	wall biosynthesis, nitrogen and/or carbon metabolism or they function as
CC	transcription factors. This polynucleotide sequence is the cress cDNA
CC	upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
CC	transcription factor, given in an exemplification of the invention.
XX	
SQ	Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
Query Match 44.0%; Score 710.4; DB 12; Length 1143;	
Best Local Similarity 77.1%; Pred. No. 2.1e-181;	
Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;	
QY	164 TGGATTCTGATAGGAAATGCTGCGAGCTGTTATTGAGGGAATGACGCTGTACTGTGTC 223
DB	
QY	2 TGGCTGATGATAGGAGATGCCCTGCTGCTGTAGTTCATGACATGATCAAGTCACCTGGTC 61
DB	
QY	224 ATATCAATTTCCACTACTATAGGAGGCAAAACGGCGCAACAAAGCAGACATATTAGTTACA 283
DB	
QY	62 ATATTATTTCCACCACAATCGGTGGCAAAATGTTGAACCAAAACAGACAATTAGTTACA 121
DB	
QY	284 TGGCTGAGCGGGTGTGGACAGGTTCAATTCGGGATGTTTTCAGGCGAATGCTTGG 343
DB	
QY	122 TGGCGGAGCGAGTGTGTGTACAGGCTGCTGCTGCGGATCGTTTCCAGCAAAATGTTGG 181
DB	
QY	344 AAATCGAGAAATCAGTAGGCATTAATAAAGTCTTTCGAAGATCGACGCTATAAAACCGTG 403
DB	
QY	182 AGACTGGAGAAACCGTGGCGATAAAGAGTGTTCGAAGATGAAGATACAGAACCGAG 241
DB	
QY	404 AGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCACTTCCTTGAAGCACTGTTTCT 463
DB	
QY	242 AACTTCAGTTGATGCGTGTGATGGATCCTCCGAATGCTGTTGTTGAAGCACTGCTTCT 301
DB	
QY	464 TCCTACACAGGTAGAGTAGCTCTCTCAACCTGTTTGAAGTATGATGATGATGATGATG 523
DB	
QY	302 TTTGAGCTACAAGTAAGACGAGCTTTCTTGAACCTTGGTTATGAGGATGATGCCCTGGA 361
DB	
QY	524 CTTTATACCGGGTTTGGAGCACTATCTAGTTCTTAATCAGAGATGCCAAATTTTCTATG 583
DB	
QY	362 GCTTGTATCGAGTTCTGAAACATATATAGTAGTCAAAACCAAGATGCTTGTCTATG 421
DB	
QY	584 TCAAGCTTTACATATCAAACTTTAGAGGTTTGGCTTACATCCATATGTTCCCGGTG 643
DB	
QY	422 TTAACCTTTACATGATATCAGATCTCCGGGAGCTTGCTTACATTCACAATGTTGCTGGAG 481
DB	
QY	644 TTTGCCACAGAGATGTGAAACCAAAATCTCTTGGTGTATCCCTTGACCCATCAGGTTA 703
DB	
QY	482 TTTGTACAGAGATCTAAGACCTCAAAATCTCTGTTGATCTCTTACTCATCAAGTCA 541
DB	
QY	704 AGCTGTGTGATTTTGGAAAGTGCAAAAGTATTGTGTCAAAGTGCAACCAATATCATATA 763
DB	
QY	542 AAATCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGTGAAGCCACATTTCTTACA 601
DB	
QY	764 TCTGCTCCCGTATATATGCGTCCAGAACTCATCTTTGGCGCAACAGAGTATACAGCAT 823
DB	
QY	602 TCTGCTCACGATTTCTACCGGTGACCCGAGCTCATATTTTGGTGCCACTGAGTACACAATT 661
DB	
QY	824 CCATAGATATAGCTGCTGCTGTTGTGCTACTGCGAGAGCTTCTTCTGGCCAGCCGTTAT 883
DB	
QY	662 CTATTGATATCTGGTCTGCTGCTGTTGTTCTTCTGCTGAGCTTCTTCTGTTGGTCAGCCATTAT 721
DB	
QY	884 TTTCCAGGAGAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA 943
DB	
QY	722 TTCCCGGAGAAAATGCTGTGATCAGCTCGTTGAAATATAAAGTTCTTGGTACACCAA 781
DB	
QY	944 CTGCTGAAGAAAATTCGATGATGAACCCGAACTACACAGATTTTAGTTCCCAACAATCA 1003
DB	
QY	782 CTCGAGAAGAAAATCCGTTGTATGAATCCATTTACACAGATTTTCAGGTTTCCACAGATAA 841
DB	

QY	1004 AAGCTCACCTTGGCACAAAGGTTTTTTCATAAACGATGCTCCAGAAGCAATAGACCTTG 1063
DB	
QY	842 AGGCATATCCCTGGCACAAAGATCTTCCCAAAAGATGCCCCCAGAGCGATGATTTTG 901
DB	
QY	1064 CATCTCGGCTTCTTCAATATTCCCAAGTCTACGCTGCACCTCGCTCGAAGCATGTGCTC 1123
DB	
QY	902 CATCAAGGCTGCTTCAATACTCTCCAAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCAC 961
DB	
QY	1124 ATCCGTTTTTCAATGAACCTCCAGAGCCAAACGCGCTTTCCAAATGCTGCTCCATTAC 1183
DB	
QY	962 ATCCGTTCTTGTGAATCACTCAGAGAACCAACGCTCGTTTACCAATGACGCGCTTTC 1021
DB	
QY	1184 GCGCATTTGTTCAATTTCAAAACAGAGTATTAGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243
DB	
QY	1022 CCGCTCTCTTCAATCTTCAAAAGAGTAGCTGGATCATCAGCTGACTGATGCTGATCAAGT 1081
DB	
QY	1244 TAATACCTGAGCATGTGAGACGACCAAAATGAGCAGGATTT 1283
DB	
QY	1082 TGATTCAGACCATATCAAGAGACAATTTGGTCTAAGCTT 1121
DB	
RESULT 8	
AAL54221	
ID	AAL54221 standard; cDNA; 1490 BP.
XX	
AC	AAL54221;
XX	
DT	27-MAR-2003 (first entry)
XX	
DE	cDNA of wild-type DWf12 protein.
XX	
KW	DWARF12; DWf12; transgenic plant; plant breeding; industrial application;
KW	agricultural production; gene; ss.
XX	
OS	Unidentified.
XX	
EH	Location/Qualifiers
CDS	200..1312
FT	/tag= a
FT	/product= "Protein of wild-type DW12 locus"
XX	
PN	WO200292777-A2.
XX	
PD	21-NOV-2002.
XX	
PF	15-MAY-2002; 2002WO-US015563.
XX	
PR	16-MAY-2001; 2001US-0291342P.
XX	
PA	(ARIZ-) ARIZONA BOARD OF REGENTS.
XX	
PI	Choe S, Feldmann K, Tax F;
XX	
DR	WPI; 2003-129285/12.
XX	
DR	P-PSDB; AAO26726, AAO26727.
XX	
PT	New isolated DWARF12 mutant polypeptide for producing transgenic plants
PT	displaying altered biochemistry, structure or morphology which are useful
PT	in plant breeding, in agricultural production or industrial applications.
XX	
PS	Example 2; Fig 2; 62pp; English.
XX	
CC	The invention relates to an isolated DWARF12 (DWf12) mutant polypeptide.
CC	The mutant polypeptide comprises at least 70 % sequence identity to the
CC	amino acid sequence of the DWf12 polypeptide given in the specification
CC	at positions 38-326 or 1-380, and having a mutation of at least one non-
CC	conservative substitution, addition or deletion of an amino acid in a
CC	region of the polypeptide corresponding to a region given in the
CC	specification. The mutant DWf12 polypeptide is useful in producing
CC	transgenic plants that display at least one altered DWf12 phenotype, such
CC	as altered biochemistry, structure or morphology. The transgenic plant
CC	can be used in plant breeding or directly in agricultural production or

CC	industrial applications. The polynucleotide is useful in isolating or
CC	creating other mutant cell gene alleles, in inhibiting or enhancing
CC	endogenous DWF12 gene expression, and in standard diagnostic assays as
CC	hybridisation probe or primer. This polynucleotide sequence represents
CC	the cDNA of the wild-type DWF12 locus of the invention
XX	
SQ	Sequence 1490 BP; 413 A; 340 C; 297 G; 440 T; 0 U; 0 Other;
	Query Match 44.0%; Score 710.4; DB 10; Length 1490;
	Best Local Similarity 77.1%; Pred. No. 2.3e-181;
	Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY	164 TGGATTCTGATAAGGAATGTCGACGCTGTATTGAGGGAATGACGCTGTACTGGTC 223
Db	201 TGGCTGATGATAGGAGATGCTCTGCTGTAGTTGATGGACATGATCAAGTCATCGTC 260
QY	224 ATATCATTTCCACCTACTATAGGAGCGCAAAACGCGCAACCAAGACGACCAATTAGTTTACA 283
Db	261 ATATTATTTCCACCACCAATCGGTGGCAAAATGTTGAACCAACAGCAATTAGTTTACA 320
QY	284 TGGCTGAGCGGTTGTTGGAAACAGGTTTCATTTCGGGATTTGTTTTTCAGCGCGAAATGCTTTGG 343
Db	321 TGCGGAGCGAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTTCCAGCAAAATGTTTGG 380
QY	344 AAACCTGAGGAATCAGTAGCCCAATTTAAAAGGCTTTGCAAGATCGACGCTATAAAAAACGGT 403
Db	381. AGACTGGAGAAACCGTGGCGATAAAGAGGTTTTTGCAAGATAGAAGATACAAGAACCAG 440
QY	404 AGTTGCAACTAATCGGACCAATGATCACCAAAATGTCATCTCTTCAGACGACGTGTTCT 463
Db	441 AACTTTCAGTTGATCGGTGATGATCATCCGAATGTGGTTGTTTGAAGCATTTGCTTTCT 500
QY	464 TCTCTACAAACGAGTAGAGATGAGCTCTTCCTCAACCTTGTATTGAGATGTACTCTGAGA 523
Db	501 TTTTCGACTACAAGTAAAGACGAGCTTTTCTTGAACCTTGGTTATGAGATGTGCTCTGAGA 560
QY	524 CTTTATACCGGTTTTTGAGGCACATATACTAGTTCTTAATTCAGAGGATGCCAAATTTTCTATG 583
Db	561 GCTTGTATCAGTTTCTGAAAACATTTATAGTAGTGCAAAACCAAGAATGCTCTTCTGTCTATG 620
QY	584 TCAAGCTTTTACACATATCAAACTTTTAGAGGTTTTGGCTTACATCCATCTATGTTCCCGGTG 643
Db	621 TTAACCTTTTACATGTATCAGATCTTCGGGGAGCTTGCTTTACATTTCAAAATGTTGCTGGAG 680
QY	644 TTTGCCACAGAGATGTGAAACCAAAAATCTCTTGGTTGATGCCCTTGACCCCATCAGGTTA 703
Db	681 TTTGTACAGAGATCTAAGCCTCAAAATCTTCTGGTTGATCTCTTACTCATCAAGTCA 740
QY	704 AGCTGTGTGATTTTGGAAAGTGCAAAAGTATTTGGTCAAAAGGTGAACCAAAACATATCATATA 763
Db	741 AAATCTCTGACTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAAGCCAAATTTCTTTACA 800
QY	764 TCTGCTCCGGTTATTATTCGTGCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCAT 823
Db	801 TCTGCTCACGATTCATCCGTCACCCGAGCTCATATTTTGGTGGCCATCGAGTACACAACCTT 860
QY	824 CCATAGATATATGCTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCACGCGGTTAT 883
Db	861 CTAATTGATATCTGGTCTGCTGGTTGTGTCTTGTCTGAGCTTCTTCTTGGTGCAGCCATTAT 920
QY	884 TTCAGGAGAAAATTCAGTTGTATCAGCTTTGTGGAGATCATAAAGGTTCTTTGGTATCTCCAA 943
Db	921 TTTCCGGAGAAAATGCTGTGATCAGCTCGTTTGAATTTATAAAAGTTCTTTGGTACACCAA 980
QY	944 CTGCTGAAGAAAATTCGATGTATGAAACCGGAACCTACACAGATTTTGTAGTTTCCCACAAAATCA 1003
Db	981 CTCGAGAAGAAAATCCGTTGTATGAATCCACATTTACACAGATTTTCAGGTTTTCCACAGATAA 1040
QY	1004 AAGCTCACCCCTTGGCACAAAGGTTTTTTCATAAAACGGATGCCCTCCAGAAAGCAATAGACCTTG 1063
Db	1041 AGGCACATCTCTGGCACAAAGATCTTCCAAAAGGATGCCCCCAAGACGCAATGATTTTG 1100
QY	1064 CATCTCGGCTTCTTTCAAATATTTCACCAAGTCTTACGCTGCATCGCGCTCGAAGCATGTGCTC 1123

PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 16-JUN-1999; 99US-0139453P.  
 PR 17-JUN-1999; 99US-0139453P.  
 PR 18-JUN-1999; 99US-0139452P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
 PR 18-JUN-1999; 99US-0139457P.  
 PR 18-JUN-1999; 99US-0139458P.  
 PR 18-JUN-1999; 99US-0139459P.  
 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 18-JUN-1999; 99US-0139763P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 21-JUN-1999; 99US-0139899P.  
 PR 22-JUN-1999; 99US-0140353P.  
 PR 23-JUN-1999; 99US-0140354P.  
 PR 24-JUN-1999; 99US-0140695P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 01-JUL-1999; 99US-0142154P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143424P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144086P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 22-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 28-JUL-1999; 99US-0145951P.  
 PR 02-AUG-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.  
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 PR 04-AUG-1999; 99US-0147038P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 04-AUG-1999; 99US-0147302P.

PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147260P.  
 PR 06-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147416P.  
 PR 09-AUG-1999; 99US-0147493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 18-AUG-1999; 99US-0149426P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149929P.  
 PR 23-AUG-1999; 99US-0149902P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0155659P.  
 PR 28-SEP-1999; 99US-0156458P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158232P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159293P.  
 PR 13-OCT-1999; 99US-0159294P.  
 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.  
 PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
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 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160980P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 23-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
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 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161992P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

		Query Match		44.0%; Score 710.4; DB 3; Length 1745;					
		Best Local Similarity		77.1%; Pred. No. 2.5e-181;					
		Matches 864; Conservative		0; Mismatches 256; Indels		0; Gaps			
QY	164	TGATTTCTGATAGGAAATGTCTGACGCTGTATTGAGGGAATACGCTGTACTGGTC	223						
DB	174	TGCTGATGATGAGGATGCTGCTGCTGTAGTGTGATGAGCATGATCAAGTCACTGGTC	233						
QY	224	ATATCATTTTCCACTACTATAGAGGCAAAACCGGCAACAAAGCAGACCAATTAATTACA	283						
DB	234	ATATTATTTCCACCACCAATCGGTGGCAAAATGGTGAACCAAAACAGACAATTAAGTTACA	293						
QY	284	TGGCTGACGGGTTCTTGAACAGGTTCAATTCGGGATTTGTTTTCAGGGAATGCTTGG	343						
DB	294	TGGCGAGCGAGTTGTGTGTACAGCTCGTTCGGGATCGTTTTTCAAGCAAAATGTTGG	353						
QY	344	AAACTGGAGAAATCAGTAGCCATTAATAAGGCTCTGCAAGATCGACGCTATAAAACCGTG	403						
DB	354	AGACTGGAGAAACCGTGGGATTAAGAGGTTTTCGACATAGAGATACAGAACCAG	413						
QY	404	AGTTGCAACTAATGCGACCAATGGAATCAACCCAAATGTCTATCTCTTGAAGCACTGTTCT	463						
DB	414	AACTTCAGTTGATGCTGTGATGGATCATCCGAATGTGGTTGTTGAAGCATTCCTTCT	473						
QY	464	TCTCTACACGAGTAGAGATGAGCTTCTCCTCAACCTTGTATGAGATGTACCTGAGA	523						
DB	474	TTTCGACTACAAAGTAAGACGAGCTTTCTTGAACCTTGTGTATGAGATGTGCTCTGAGA	533						
QY	524	CTTTATACCGGTTTGTAGGCACTACTACTAGTCTTAATCAGAGGATGCCAATTTCTATG	583						
DB	534	GCTTGTATGAGTTCTGAAACATTAATAGTAGTGCAACCAAGAAATGCTCTTGTCTATG	593						
QY	584	TCAAGCTTTTACACATATCAAAATCTTTAGAGGTTTGGCTTTACATCCATATGTTCCCGGTG	643						
DB	594	TTAAACTTTTACATGATCAGATCTTCCGGGACTTGTCTTACATTCACAATGTTGCTGGAG	653						
QY	644	TTTGCCACAGAGATGTAACCAACAATCTCTTGGTTGATCCCTTGACCCATCAGTTA	703						
DB	654	TTTGTACAGAGATCTAAAGCCCTCAAAATCTTCTGGTTGATCTCTTACTCATCAAGTCA	713						
QY	704	AGCTGTGTGATTTTGGAGTGAAGATATTGTCGTAAGGTGAACCAACATATCATATA	763						
DB	714	AAATCTGTGACTTTGGGAGTGGCAACAGCTCGTTAAAGTGAAGCCAACTTTCTTACA	773						
QY	764	TCTGCTCCCGTTATATCGTGTCCAGAACTCATCTTTGGGCCACAGAGTATACAGCAT	823						
DB	774	TCTGCTCAGGATTTACCGTGCACCCGAGCTCATATTTGGTGCCACTGAGTACACAAT	833						
QY	824	CAATAGATATATGCTGTGCTGTGTGTGTAAGTGTGAGAGAGCTTCTTGTGGCCAGCGTTAT	883						
DB	834	CTATTGATATCTGCTGTGCTGTGTTCTTGTCTGAGCTTCTTGTGTCAGCCATTAT	893						
QY	884	TTCCAGGAGAAATTCAGTTGATCAGCTGTGAGATCATATAAGTCTTGTGACTCCAA	943						
DB	894	TTCCCGGAGAAATGCTGTGGATCAGCTGTGTGAATATATAAGTTCTTGTGACACCA	953						
QY	944	CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTGGTTCCCAAAATCA	1003						
DB	954	CTCGAGAGAAATCCGTTGATGAATCCACATTAACAGATTTTCAAGTTTCCACAGATA	1013						
QY	1004	AACTCACCCTTGGCAGCAAGGTTTTTATTAACGATGCTCCAGAGCAATAGACCTTG	1063						
DB	1014	AGGCATATCCCTTGGCAGCAAGATCTTCCAAAGAGTATGCCCCAGAGCGATTTGATTG	1073						
QY	1064	CATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCATGTGTC	1123						
DB	1074	CATCAAGGCTGCTTCAATATCTTCAAGTCTTAAGATGCAAGCGCTTCAAGCTTGTGAC	1133						
QY	1124	ATCCGCTTTTCAATGAATCTCCGAGCCAAACCGCCGCTTCTTCAATGCTGCTCATTTAC	1183						
DB	1134	ATCCGCTTTTCAATGAATCTCCGAGCCAAACCGCTGCTTCAATGCTGCTCATTTAC	1193						
QY	1184	CGCCATTTGTTCAATTTTCAACAAAGATTTAGTGGAGCTTCAATGAGGCTTAATCAACAGGC	1243						

DB	1194	CGCTCTCTTCAACTTCAACAAGAGTAGTGGATCATACCTGAACTGGTCAACAAGT	1253						
QY	1244	TAATACCTGAGCATGTGAGACGACAAATGACACAGGATT	1283						
DB	1254	TGATTCAGACCATATCAAGAGACAATTTGGTCTAAGCTT	1293						
RESULT 10									
ID	AAH47004	standard; cDNA; 1673 BP.							
XX	AAH47004;								
AC	AAH47004;								
XX	29-OCT-2001	(first entry)							
XX	Wheat glycogen synthase kinase-3 cDNA.								
XX	Protein kinase; calcium-dependent phosphorylase kinase; CDPK; GSK-3;								
KW	glycogen synthase kinase-3; GSK; ss.								
OS	Triticum aestivum.								
FH	Key	Location/Qualifiers							
FT	CDS	44..1252							
FT	/*tag= a	/product= "wheat GSK-3"							
XX	US262345-B1.								
PN	17-JUL-2001.								
PD	02-JUL-1999;	99US-00347801.							
PF	10-JUL-1998;	98US-0092438P.							
PR	(DUPO ) DU PONT DE NEMOURS & CO E I.								
PA	Allen SM, Lee J;								
PI	WPI; 2001-440863/47.								
DR	P-FSDB; AAB85589.								
XX	New isolated polynucleotide encoding polypeptide having glycogen synthase kinase activity or its complement, useful for producing transgenic plants with altered levels of glycogen synthase kinase.								
PT	Claim 3; Col 45-48; 42pp; English.								
CC	The invention relates to protein kinases, especially calcium-dependent phosphorylase kinase (CDPK) and glycogen synthase kinase-3 (GSK-3). The polypeptides having GSK activity can be expressed by standard recombinant methodology. The polynucleotides encoding the polypeptides are useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species, for immunological screening of cDNA expression libraries, and for creating transgenic plants in which the glycogen synthase kinase polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are normally found. The polynucleotides are also useful as probes for genetically and physically mapping the genes that they are part of, and as markers for traits linked to those genes. The polypeptides are useful for altering the level of expression of GSK-3 in a transformed host cell. The present sequence represents a wheat GSK-3 cDNA								
XX	Sequence 1673 BP; 419 A; 421 C; 408 G; 424 T; 0 U; 1 Other;								
XX	Query Match	43.5%; Score 701.6; DB 5; Length 1673;							
XX	Best Local Similarity	74.7%; Pred. No. 5.9e-179;							
XX	Matches 881; Conservative	0; Mismatches 299; Indels	0; Gaps	0;					
QY	98	AGCCTCATGCTTCTGCTCGCGCTGACGCTTCAAGCGGCGACGCTTTGAACCCGTC	157						
DB	48	AGCATCCGCGCCGCGCGCGGATGCTGCTGACGAGCGCCGCCACCGCAGTCG	107						

Qy	158	CTGAATTTGGAAATCTGTATAAGAAATGCTCTGGAGCTGTATTATTGAGGGAAATGACGCTGTGTTA	217
Db	108	CCTGCGAAGAAAGACACAGATGGCGAGCGCGGTATGCGGAGGGGAACGACGCCCATGA	167
Qy	218	CTGGTCATATCATTTTCCACTACTATAGGAGCGAANAACCGGAAACGGAACCAAAACGACACCAATTA	277
Db	168	CCGGTCATCATCTCTCACCAACCATCGCGCGCAAGAAACGGCGAGCCCAAGCAGACGANTTA	227
Qy	278	GTTACATGGCTGAGCGGGTTGTGGAAACAGGTTCAATTCGGGATGTGTTTTTCAGGCGGAAAT	337
Db	228	GCTACATGGCGGAGCGGTTGTGGGCACTGGTTCGTTTGGCATCGTCTTTTCAGGCTAAAT	287
Qy	338	GCTTTGGAAACTGGAGAAATCAGTAGCCCAATTAATAAAGAGTCTTTCGAAGATCGACGCTATATAAA	397
Db	288	GCCTTGGAAAACCGGGGAGATGGTGGCATTAAGAAGGTACTTCGAGGACAGACGGTCAACAAG	347
Qy	398	ACCGTAGGTTGCAACTAATCGGACCAATGGATCACCCAAATGTCATCTCTCTTGAAGCACT	457
Db	348	ACCGTAGCTGCGAGCTTATGCGTTTCGAATATCCAAATTCGAATGTGTCTCCCTCAAGCACT	407
Qy	458	GTTTCTTCTCTCAACACGAGTAGAGATGAGCTCTTCTCAACCTTTGTTATGGAGTAGTGTAC	517
Db	408	GCCTCTTCTCAACCAACAAGTAGAGATGAGCTGTTCTCTGAACCTGTTCATGAGTAGTGTCC	467
Qy	518	CTGAGACTTTATACCGGGTTTGGGCACTATACTAGTTCTTAATCGAGAGATGCCAAATTT	577
Db	468	CGGAGACGCTATACCGCGTGCTTAAGCACTACAGTAAATGCAACACGAGGATGCGCGTTA	527
Qy	578	TCTATGTCAAGCTTTACACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATACACTGTTC	637
Db	528	TCTATGTCAAGCTTTTACATGATCAGCTTTTTAGAGGGCTAGCTTATGTTTCATACTGTTC	587
Qy	638	CCGGTGTTTGCCACAGAGATGTGAACCACAAATCTCTTGGTTGATCCCTTGACCCATC	697
Db	588	CAGGAGTTTGCCACAGGGATGTGAACCACAAATGTTTTGTTGATCCTCTAACCCATC	647
Qy	698	AGGTTAAGCTGTGTGATTTTGGAAAGTCGAAAAGTAATTTGGTCAAAAGGTGAACCAAAATAT	757
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Qy	758	CATATATCTGCTCCCGTTATTATCGTGCTCCAGAACTCATCTTTGGCGGCCACAGAGATATA	817
Db	708	CATACATATGCTCTCGGTACTATCGTGCTCTGAGCTCATATTTTGGTGAACATGAATATA	767
Qy	818	CAGCATCCATAGATATATGCTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTTGGCCAGC	877
Db	768	CAACTTCAATAGACATATGGTCAGCTGGATGTGTTCTTTCAGAGACTACTTCTTTGGTCAGC	827
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Qy	938	CTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTATAGGTTTCCAC	997
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Qy	1118	GTGCTCATCCGTTTTTCAATGAACTCCGAGAGCCAAAACGCGCTCTTCCAAATGGTGGCTC	1177
Db	1068	GTGCACATCTCTTCTTGAAGAGCTACGTGAGCCGAATGACGCTTGCAGATGGCGGCC	1127
Qy	1178	CATTACCGCCCATTTGTTCAATTTCAAAACAAGAGTTAGTGGAGCTTCAATGGAGCTAATCA	1237
Db	1128	CATTCCCTCTCTGTTCAACTTCAAACTGAACCTAGGGAACGCGCTCTCCAGAGCTATCA	1187

[illegible]

RESULT 11  
ABQ82534

ABQ82534  
ID ABO82534 standard: CDNA: 1673 BP.

AC ABQ82534;

DT 19-DEC-2002 (first entry)

DE wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15.

XX Glycogen synthase kinase; kinase; immunological screening;  
KW plant breeding: gene: ss.  
KW plant breeding: gene: ss.

XX  
QS  
Triticum aestivum.

XX	Key	Location/Qualifiers
FH		

FH	key	Location/
FT	CDS	44-1252

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ET
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44: .1232
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F1 /-cay- a
F2 /product= "glycogen synthase kinase"

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XX PN US2002120949-A1.

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PD  
29-AUG-2002

14-MAY-2001: 2001HS-00854731

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99US-0002438P

PR 10-JUL-1998; 98US-0092438P.  
PR 02-JUN-1999; 99US-00347801

XX  
DZ (X Y T F / ) X Y T F N C M

XX 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048

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DR WPI; 2002-731384/

XX New calcium-dependent phosphorylase kinase and glycogen synthase kinase  
PT polypeptides, for altering level of expression of kinase polypeptides in  
PT plants.

PS Claim 15: Page 22-24: 41pp: English: **XX**

The present invention describes kinase polypeptides (I) such as a calcium-dependent phosphatase kinase polypeptide comprising a sequence of 101, 623, 157 or 111 (see ABP53629 to ABP53632) amino acids, and a glycogen synthase kinase polypeptide comprising all or a portion of a sequence of 410, 105, 399 or 402 (see ABP53633 to ABP53636) amino acids. (I) is useful for immunological screening of cDNA expression libraries, and for preparing antibodies against the polypeptides, where the antibodies would be useful for detecting (I) in situ or in vitro, in cell extracts.

be useful for detecting (I) *in situ* or *in vitro*, in cell extracts. Nucleic acids (II) encoding (I) can be used to isolate cDNAs and genes encoding homologous proteins from the same or other plant species. (II) can also be used for creating transgenic plants in which (I) is present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. (II) are useful as probes or primers. The polynucleotides may be used as probes for genetically and physically mapping the genes that they are a part of and used as markers for traits linked to those genes. The information can be used in plant breeding in order to develop lines with desired phenotypes. The present sequence encodes a glycogen synthase kinase from the present invention

Sequence 1673 BP: 419 A: 421 C: 408 G: 424 T: 0 U: 1 Other: XX

Query Match 43.5%: Score 701.6: DB 6: Length 1673:

Query Match 43.5%; score 701.6; DB 87  
Best Local Similarity 74.7%; Pred. No. 5.9e-179;

BEST LOCAL SIMILARITY 74.7%; FREQ. NO: 3.3E-179;  
Matches 881: Conservative 0: Mismatches 299: Indels 0: Gaps 0:

DB T128 CATTCCTCTCTGTTCAACTTCAAAACC1GAAC1AGCGAAGCGCTCTCCAGAGGCTCATCA T187



98 AGCTCATGCTCTTCTCGCGCTGCGAGCTTCAAGCGGCGAGCGCTTTTGAACGCCGTC 157  
118 AGCTATCCGCGCGCGCGCGCGAGCGCTGCTGCTGAGAGAGCGCCGCCACCGAGTCG 107  
158 CTGAATTTGATTTCTGATAAGGAAATGTCTGACGCTGTTTATTGAGGGAATGACGCTGTTA 217  
108 CTTGCGAG 167  
218 CTGCTCATATCTTCCACTACTATAGGAGGCAAAACCGGCAACCAAGAGAGACCATTA 277  
168 CCGGTTCATATCTTCCACCATCTGCGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 227  
278 GTTACATGCTGAGCGGCTGTTGGAACAGAGTTTCAATCGGGATTTCTTTTTCAGGCGAAT 337  
228 GCTCATGCGGAGCGCGCTTGTGGGCACTGTTGCTTTGGCATGCTTTTCAGGCTAAT 287  
338 GCTTGAACCTGGAGAAATCAGTAGCCATTAATAAGGCTTTGCAAGATCGAGCTATAAAA 397  
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398 ACCGTGAGTTGCACTAATGAGCAACAAATGATGATCACCAGGATGATCTCTTGAAGCACT 457  
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458 GTTCTTCTTACACGAGTAGAGATGAGCTTCTTCAACCTTTGATGAGATGATAC 517  
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518 CTGAGACTTTTACCGGCTTTGAGGCACTACTAGTTCTTAATCAGAGGATGCCAAATTT 577  
468 CGGAGAGCTATACCGGCTTTGAGGCACTACTAGTTCTTAATCAGAGGATGCCAAATTT 527  
578 TCTATGTCAGGCTTTTACATATCAATCTTTTAGAGGTTTGGCTTTTACATCCATCTGTC 637  
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638 CCGGTGTTTGCACAGAGATGTAACCAACCAAAATCTCTTGGTTCATCCCTTGACCCATC 697  
588 CAGGAGTTTGCACAGGATGTAACCAACCAAAATGTTTGGTTCATCCCTTGACCCATC 647  
698 AGTTAAGCTGTGATTTTGAAGTGAAGTATGTTTGAAGTGAAGTGAAGTGAAGTGAAGT 757  
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758 CATATATCTGCTCCGTTTATATCTGCTTCCAGAACTCATCTTTGGCGCCACAGAGTATA 817  
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DT 17-OCT-2000 (first entry)  
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33613.  
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KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
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OS Arabidopsis thaliana.  
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FN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
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PF 25-FEB-2000; 2000EP-00301439.  
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PR 05-MAR-1999; 99US-0123180P.  
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PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
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PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	28-OCT-1999;	99US-0161361P.
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PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
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PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	08-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			

Query Match 43.3%; Score 698.4; DB 3; Length 1635;  
 Best Local Similarity 77.1%; Pred. No. 4.3e-178;  
 Matches 863; Conservative 0; Mismatches 256; Indels 1; Gaps 1;  
 QY 164 TGGATTCTGATAGGAATGCTGCAGCTGTTATTGAGGGAATGACGCTGTACTGGTC 223  
 DB 174 TGGCTGATGATAGGAGATGCCTGCTGCTAGTGTGATGACATGATCAAGTCACCTGGTC 233



Db 333 CGAAGTCTTGAGACTGCGGAGGAGTGGCTATAAAGAGGTCTTGCAGGACAGGCGAT 392  
 Qy 392 ATAAAAACCGTGAAGTGAAGTAAATCGACCAATGATGATCACCNAATGTCATCTCTTGA 451  
 Db 393 ACAAANAATCGTGAAGTGAAGTAAATCGGCGTATGATGATCACCNAATATAATTTCTCTGA 452  
 Qy 452 AGCACTGTTTCTCTCTACAACGAGTGAAGTGAAGTCTTCTCTCAACCTTGTATGAGGT 511  
 Db 453 GTAACATATTTCTCTCTACAACGAGTGAAGTGAAGTCTTCTCTCAACCTTGTATGAGGT 512  
 Qy 512 ATGTACCTGAGACTTTTATACCGGTTTTCAGGCACTATATAGTTCTTAATCAGAGGATCC 571  
 Db 513 ATGTCTCTGAGAGTCTTCTCGGTGTTATAAGCACTACAGTGAAGTGAAGTGAAGTGAAGT 572  
 Qy 572 CAATTTCTATGTCAAGCTTTACACATATCAATCTTTAGAGGTTTGGCTTATATCCATA 631  
 Db 573 CCTAATCTATGTGAATTTATATACATATCAATCTTTAGGAGCTTGGGCTATATCCATA 632  
 Qy 632 CTGTTCCCGGTGTTTCCACAGAGTGTGAACCAACCAAAATCTCTTGGTTGATCCCTTGA 691  
 Db 633 CTGTACAGGAATCTGCCATAGGAATTTGAAGCTCAAAATCTTTTGGTTGATCGACTCA 692  
 Qy 692 CCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTCAAAAGTATTTGGTCAAAAGGTGAACCA 751  
 Db 693 CACACCAAGTCAAGCTCTGTGATTTTGGAGTGCAAAAGTCTCTGTGGAGGTGAATCAA 752  
 Qy 752 ACATATCATATCTCTCTCGGTATATATCGTCTCAGAACTCATCTTTGGGCGCACAG 811  
 Db 753 ACATTTTATATATATTTTCAAGCTACTATCGTGGCCGAGAGCTTAATTTTGGTGGCGAG 812  
 Qy 812 AGTATACAGATCCATAGATATATGCTGCTGTGTTGTCTGCTGAGAGCTTCTCTTGG 871  
 Db 813 ATATACAACTCTGTGTATATTTGGTTCGCTGTTGTTGCTTGGGAACTTCTCTAG 872  
 Qy 872 GCCAGCGGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 931  
 Db 873 GCCAGCGGTTTGTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 932  
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 Db 933 TTGGCACTCTACTCGAGAAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 992  
 Qy 992 TCCCAAAATCAAGCTTCAAGCTTGGCAAGGTTTTCATAAACGAGTGCCTCCAGAAG 1051  
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 Qy 1052 CAATAGACTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1111  
 Db 1053 CAATAGACTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1112  
 Qy 1112 AAGCATGTGCTCATCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1171  
 Db 1113 AAGCATGTGCTCATCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1172  
 Qy 1172 GTGCTCCATTCACCGCATTTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1231  
 Db 1173 GTGCTCCATTCACCGCATTTTCAATATTCACCAAGTCTACGCTGCACCTGCGCTCG 1232  
 Qy 1232 TAATCAACAGGCTTAATCTCTGAGCTATGAGAGCAAAA 1270  
 Db 1233 TGCTTCTTAAGCTCATCCAGAGCATGTCTCAGGCGGCAAA 1271

RESULT 14

ACC57970

ID ACC57970 standard; cdna; 1621 BP.

XX ACC57970;

AC ACC57970;

XX 11-AUG-2003 (first entry)

DE Canola protein kinase stress-related polypeptide BnPK-2 cDNA.

XX BnPK-2; protein kinase stress-related polypeptide; PKSRP; enzyme;  
 KW transgenic plant; plant; stress tolerance; drought tolerance;  
 KW salt tolerance; cold tolerance; canola; gene; ss.  
 OS Brassica napus.  
 XX Key Location/Qualifiers  
 FT 132..1277  
 FT /tag= a  
 FT /product= "BnPK-2"  
 XX WO2003040171-A2.  
 XX 15-MAY-2003.  
 XX 12-NOV-2002; 2002WO-US036374.  
 XX 09-NOV-2001; 2001US-0346096P.  
 XX (BADI ) BASF PLANT SCI GMBH.  
 XX Van Thiel N, Da Costa E SilvaO, Chen R;  
 XX WPI; 2003-441522/41.  
 XX P-PSDB; ABR42363.  
 XX New protein kinase stress-related polypeptide coding nucleic acid, useful  
 PT for producing transgenic plants with an increased tolerance to an  
 PT environmental stress, e.g. high salinity, as compared to a wild type  
 PT variety of the plant.  
 XX Claim 1; Page 90-91; 111pp; English.  
 CC The present sequence is a full-length cDNA encoding BnPK-2, a novel  
 CC canola protein kinase stress-related polypeptide (PKSRP). The cDNA was  
 CC identified on the basis of homology to Physcomitrella patens PK-3 (see  
 CC ACC57962) and PK-10 (see ACC57966) sequence. BnPK-2 is an example of  
 CC PKSRPs of the invention that are important for modulating a plant's  
 CC response to environmental stress. Over-expression of PKSRP coding nucleic  
 CC acids in a plant results in the plant's increased tolerance to  
 CC environmental stress. Transgenic monocot and dicot plants are provided  
 CC that show increased tolerance to high salinity, drought and low  
 CC temperature  
 XX Sequence 1621 BP; 450 A; 371 C; 331 G; 469 T; 0 U; 0 Other;  
 SQ  
 Query Match 42.1%; Score 678.8; DB 8; Length 1621;  
 Best Local Similarity 74.5%; Pred. No. 8.6e-173;  
 Matches 854; Conservative 0; Mismatches 292; Indels 0; Gaps 0;  
 Qy 183 GTCTCAGCTGTATTGAGGAAATCAGCTGTACTGCTCATATCATTTCCACTACTAT 242  
 Db 155 GCGGCTGTCTGTAGTTGATGGACATGACCAAGTCTGCGCCACATAATCTCCACCACCAT 214  
 Qy 243 AGGAGCAAAAACGGCAACCAAGCAGACCACTAGTTACATGCTGAGCGGTTGTGG 302  
 Db 215 CGTGTGTAACCGGAGAACCAACAGACATAAGTTACATGCGGAGCGAGTTGTGG 274  
 Qy 303 AACAGTTTCATTCGGGATTTGTTTTCAGGCGAAATGCTTTGGAACCTGGAGAAATCAGTAGC 362  
 Db 275 TACAGGCTCTTTCGGGATAGTTTTCAGGCGAAATGCTTCTGGAGACTGGAGAAACCGTGGC 334  
 Qy 363 CATTAAAGGTTCTTCAAGATCGAGCTATAAACCGGTTCGAACTATATGCGACC 422  
 Db 335 GATAAAGAGGTTTTCAGAGCAGGAGGTACAGAACCGGAGCTTCAGCTGATGCTGT 394  
 Qy 423 AATGATCACCAAAATGTCATCTCTTGAAGCACTGTTTCTTCTCTACCAACGAGTAGAGA 482  
 Db 395 GATGGACCATCGAATGTTGTTTGTGTTGAGCATTCGTTCTTCTCGACCGAGCAAGA 454  
 Qy 483 TGAGCTCTTCTCAACCTTGTATGAGGATGTGATCTGAGACTTTATATCCGGGTTTGTAG 542



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PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.	Matches	833;	Conservative	0;	Mismatches 267;
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PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.					0;
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.	QY	185	CTGCAGCTGTTATTGAGGGAATGACGCTGTTTACTGGTTCATATCATTTCCACTACTATAG	244	Gaps
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.	Db	168	CTGGTTCTATGATTGAAGGGAGTGATCCGGTTCACAGGCCATATAATCTCGACAACCATTG	227	
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.	QY	245	GAGGCAAAACCGCGNACCAAGACGACCATTAGTTACATGGCTGACGGGTTGTTGGAA	304	
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.	Db	228	GAGGGAAGAAATGGAGAGCCTTAAAGACTATCAGCTACATGGCAGAGAGATTGTGGAA	287	
PR	14-JUL-1999;	99US-0143624P.	PR	06-OCT-1999;	99US-0157753P.	QY	305	CAGGTTCAITTCGGGATTGTTTTTCAGGCGAAATGCTTGGAACTGAGAACTGAGATCAGTAGCCA	364	
PR	15-JUL-1999;	99US-0144005P.	PR	07-OCT-1999;	99US-0157865P.	Db	288	CTGGATCAITTTGGAAATCGTCTTCCAGGCAAAATGCTCGAGACTGTTGAGACTGTTGCGA	347	
PR	16-JUL-1999;	99US-0144085P.	PR	08-OCT-1999;	99US-0158029P.	QY	365	TTAAAAAGGCTTTCGAAGATCGACGCTATATAAAACCGTGAAGTTGCAACTTAATCGCACCA	424	
PR	19-JUL-1999;	99US-0144086P.	PR	12-OCT-1999;	99US-0158369P.	Db	348	TTAAGAAGGTTTTGCAAGCAACGCGCTACAAGAACAGGAGCTTACAAATCATCGCATCCA	407	
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.	QY	425	TGGATCACCBAATGTCATCTCGTTGAAGCACTGTTTCTTCTCTACACAGAGTAGAGATG	484	
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.	Db	408	TGGATCACTGCAATGTTGTTTCTTCTTGAAGCAATGCTTCTTCTTCTTACCAACAGCAGATG	467	
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.	QY	485	AGCTCTTCCTCAACCTTGTATTGAGATGTTACTCGAGACTTTTATACCGGGTTTTCAGGC	544	
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PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159638P.					
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.					
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.					
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.					
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160768P.					
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160770P.					
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160814P.					
PR	23-JUL-1999;	99US-0145145P.	PR	21-OCT-1999;	99US-0160815P.					
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160980P.					
PR	23-JUL-1999;	99US-0145219P.	PR	22-OCT-1999;	99US-0160981P.					
PR	26-JUL-1999;	99US-0145276P.	PR	22-OCT-1999;	99US-0160989P.					
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161404P.					
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PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161992P.					
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.					
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PR	01-SEP-1999;	99US-0151530P.								
PR	07-SEP-1999;	99US-0152363P.								
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PR	13-SEP-1999;	99US-0153758P.								

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Qy	665	CACAAATCTCTTGGTGTGATCCCTTGACCCATCAGGTTAAGCTGTGATTTTGGAGTG	724
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Qy	725	CAAAAGTATTTGCTAAAGTGAAACCAACATATCATATATCTGCTCCCGTTATTATCGTG	784
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Qy	785	CTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATATGTTGCTG	844
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Qy	845	GTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGCGCTTATTTCCAGAGAAAATTCAGTTG	904
Db	828	GATGTGTTCTTGTGAGCTGCTTCTTGGCCAGCGCTCTCTTCCCTGGTGAAGTGTGTGG	887
Qy	905	ATCAGCTTGTGAGATCATAAAGTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTA	964
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Qy	965	TGAACCCGAACTPACACAGATTTAGGTTCCCAAAATCAAAGCTCACCTTGGCCAAAG	1024
Db	948	TGAATCCAAACTPACACCGAGTTTAGATTTCTCTCAGATCAAAGCTCACCCATGGCACAAGA	1007
Qy	1025	TTTTTTCATAACGGATGCTCCAGAACATAGACCTTGCATCTCGGCTTCTTCAATATT	1084
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Qy	1085	CACCAAGTCTACGCTGCCTCGGCTCGAAGCATGTGCTCATCCGTTTTTCAATGAATCC	1144
Db	1068	CACCAATCTAAGATGCACTGCTCTTGAAGCGTGTGCATCCATCTTTGACGATTTGC	1127
Qy	1145	GAGAGCCAAACGCCGCTCTTCCAAATGGTGTGCTTACCGCCATTTGTTCAATTTCAAAC	1204
Db	1128	GAGAACCAATGCGAGGTTGCCAAATGGAGCGCCATTTCTCCACTGTTCACTTTAAAC	1187
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Search completed: June 23, 2005, 11:47:05  
Job time : 1268.83 secs

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1	972.2	60.2	1636	4	US-09-578-194-6	Sequence 6, Appli
2	701.6	43.5	1673	3	US-09-347-801-15	Sequence 15, Appl
3	701.6	43.5	1673	4	US-09-854-731-15	Sequence 15, Appl
4	549.8	34.1	1814	3	US-09-347-801-9	Sequence 9, Appli
5	549.8	34.1	1814	4	US-09-854-731-9	Sequence 9, Appli
6	523.4	32.4	1429	3	US-09-347-801-13	Sequence 13, Appl
7	523.4	32.4	1429	4	US-09-854-731-13	Sequence 13, Appl
8	385.2	23.9	1389	3	US-09-489-765A-3	Sequence 3, Appli
9	385.2	23.9	1389	4	US-09-016-434-1414	Sequence 1414, Ap
10	384.4	23.8	2088	2	US-08-602-264A-1	Sequence 1, Appli
11	384.4	23.8	2088	3	US-08-461-018A-1	Sequence 1, Appli
12	384.4	23.8	2088	3	US-09-216-958-1	Sequence 1, Appli
13	375.8	23.3	1952	4	US-09-566-921-24	Sequence 24, Appl
14	375.8	23.3	2154	3	US-09-488-856A-3	Sequence 3, Appli
15	373.8	23.2	1972	2	US-08-602-264A-2	Sequence 2, Appli
16	373.8	23.2	1972	3	US-08-461-018A-2	Sequence 2, Appli
17	373.8	23.2	1972	3	US-09-216-958-2	Sequence 2, Appli
18	290	18.0	1185	4	US-09-248-796A-4396	Sequence 4396, Ap
19	172	10.7	304	4	US-09-313-294A-6825	Sequence 6825, Ap
20	154	9.5	286	4	US-09-313-294A-2895	Sequence 2895, Ap
21	133.8	8.3	305	4	US-09-313-294A-5874	Sequence 5874, Ap
22	120.2	7.4	1236	4	US-09-248-796A-4397	Sequence 4397, Ap
23	113.6	7.0	584	3	US-09-347-801-11	Sequence 11, Appl
24	113.6	7.0	584	4	US-09-854-731-11	Sequence 11, Appl
25	106.2	6.6	272	4	US-09-313-294A-6721	Sequence 6721, Ap
26	103	6.4	275	4	US-09-313-294A-1703	Sequence 1703, Ap
27	94.6	5.9	479	2	US-08-602-264A-13	Sequence 13, Appl

QY 151 CGCGCTCTGAATTTGATTTCTGATAGGAAATGCTCTGACAGCTGTTATTTCAGGGAATGAC 210  
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 QY 129 CGTCGTCGCGATATAGCAACCAAGGAATGCTGCTGCTGTTATAGGAATGAT 188  
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 QY 211 GCTGTTACTGCTCATATCTTCTCACTACTATAGGAGCAAAACCGCGAAACCAAGCAG 270  
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 QY 249 ACCATTAGTTACATGCGCGCAACGTTGTTGGAACAGAGTCAATTCGGAATTTGTTTCCAG 308  
 Db |||||  
 QY 331 GCGAAATGCTTGAAACTCGGAATCAGTAGCCATTAATAAAGTCTTTCGAAGATCGAGCG 390  
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 QY 309 GCAAAATGCTTGGAACTCGGAATCAGTAGCCATTAATAAAGTCTTTCGAAGATCGCGT 368  
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 QY 391 TATAAAACCGGTGAGTTGCAACTTAATGCGACCAATGGATCACCCAAATGCTATCTCCTTG 450  
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 QY 369 TATAAAACCGGAGTTGCAATTAATGCGACTAAATGACCATCCAAATGTTGTTCTTG 428  
 Db |||||  
 QY 451 AAGCACTGTTTCTTCTCAACGAGTAGAGATGAGCTCTTCTCAACCTTGTATTGGAG 510  
 Db |||||  
 QY 429 AAGCAATGTTTCTTCTCAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAG 488  
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 QY 511 TATGTACCTGAGACTTTATACCGGTTTTCGAGCACTATAGTTCTTAATCAGAGGATG 570  
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 QY 489 TATGTACCAAGACATTTGACCGGTTTTCGAGCACTATAGTTTCAACACAGCGGATG 548  
 Db |||||  
 QY 571 CCAATTTTCTATGCTCAAGCTTTTACACATATCAAACTTTTAGAGGTTTGGCTTACATCCAT 630  
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 QY 549 CCTATCTTCTATGCTCAAACTTTTACACATACCAAACTTTCAGAGCTTGGCTTATATCCAT 608  
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 QY 631 ACTGTTCCCGGTTGTTGCCACAGAGATGGAACCAAAATCTCTGTTGTTGATTCCTTG 690  
 Db |||||  
 QY 609 ACTGCTCCTGTTGTTGCCACAGAGATATAAAACCAAAATCTTTCGTTGATTCCTCCAC 668  
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 QY 691 ACCCATCAGTTAAGCTGTGATTTTGAAGTGCAAAAGTATGCTCAAGGTGAACCA 750  
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 QY 751 AACATATCATATATCTGCTCCGCTTATATGCTGCTCCAGAACTCATCTTTGCGCGCAC 810  
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 QY 871 GGCAGCGCTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGGTT 930  
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 QY 849 GGCAGCGCTTATTTCCGGGAGAAATTTCTGTCAGCAGCTAGTGTGAGATCATATAAGGTT 908  
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 QY 909 CTTGTTACTCCAACTCGTGAGAAATTCGCTGTCATGAACCCAACTACACAGATTTTACA 968  
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 QY 969 TTCCCAAAATCAAAAGCACCCTTGGCATTAAGGTTTTCACAAAGCGATGCTTCCGGAA 1028  
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 QY 1029 GCAATGACCTTGCATCTCGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGCGCTC 1088  
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 QY 1089 GAGGCATGTGCGCATCCGTTTTCATGAACTCCGTTGAGCAAAATGCTGCTCTTCCAAAT 1148  
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 QY 1171 GGTGCTCATTTACCGCATTTGTTCAATTTCAAAACAAGATTAGGTGAGGCTTCAATGGAG 1230  
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 QY 1149 GGCAGCACTTACACCGTTGTTCACTTCAAAACAAGATTGTTGCGGGCTTCCACCGGAG 1208  
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QY 1231 CTAATCAACAGGCTAATACCTGAGCATGTGACAGCAAAATGAGCACAGGATTTACAAAAC 1290  
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 QY 1209 CTTATCAACAGGCTAATACCGAGCATGTGAGCGGACAGATCAATGGTGGCTTTCCATTT 1268  
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 QY 1291 AGTTAAAAAC-----TGTGCATGCTCTGAAGAGAAAGAGAGGAGAAAG 1331  
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 QY 1269 CAAGCTGGACCTCGAAAAGCGATCTCGAGATGCTTTTTCAGAGCAAAATGCGGCTTAT 1328  
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 QY 1332 CAGGTTTACTACTTTTATTTGATAGTTTACAGGTTTCAACAGTATATTAACACGACTATT 1391  
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 QY 1329 GGAATGAAGGAGAGGAGATTTTACTTCTCTGATTAACATAGATATCAGCTTCTTGAGAAG 1388  
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 QY 1392 ATCAGCTTCTATACCCGCTAGTAAAGTCAATTTTTCAGCTTTTTCAGAAATCAGATGCTGATA 1451  
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 QY 1389 AGATGATGCTCTCTCTTAGACGTCGCCAAATTCAGCTTTTTCAGAAATCAGGAGGCGATG 1448  
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 QY 1452 ATGCGTCTATTTTCTTTTATCTTAGCTTGGAGAGTGGAGAGAGACACTGTTCTCTCG 1511  
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 QY 1449 ATTGTGTCCTTATAATCTTTTGTCTCACTGACTTGTAGAGAGATACTTTTCTCTCTGTA 1508  
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 QY 1569 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1611  
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RESULT 2

US-09-347-801-15  
 ; Sequence 15, Application US/09347801  
 ; Patent No. 6262345  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Allen, Steve  
 ; APPLICANT: Lee, Jian Ming  
 ; TITLE OF INVENTION: Plant Protein Kinases  
 ; FILE REFERENCE: BB-1171  
 ; CURRENT APPLICATION NUMBER: US/09/347,801  
 ; CURRENT FILING DATE: 1999-07-02  
 ; EARLIER APPLICATION NUMBER: 60/092,438  
 ; EARLIER FILING DATE: July 10, 1998  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 15  
 ; LENGTH: 1673  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1349)  
 US-09-347-801-15

Query Match 43.5%; Score 701.6; DB 3; Length 1673;  
 Best Local Similarity 74.7%; Pred. No. 3.5e-200;  
 Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 98 AGCTCATGCTTGTGCTCGCGCTGACGCTTCAAGCGGCGAGCTTTTGAACGCGGTC 157  
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 QY 48 AGCATCCGCGCGCGCGCGAGCGGATGCTGCTGACGAGCAGCGCCCAACCGCAGTCG 107  
 Db |||||  
 QY 158 CTGAATTGATTTCTGATAAGGAAATGCTCTGACGCTGTTATTGAGGGAATGACGCTGTTA 217  
 Db |||||  
 QY 108 CTGCGAAGAGAGAGAGAGGATGGCGAGCGCGCTGATCGGAGGGAGACGACCCATGA 167  
 Db |||||  
 QY 218 CTGGTCATATCATTTTCCACTACTATAGGAGGCAAAACCGCGAACCAAGCAGACCATTA 277  
 Db |||||  
 QY 168 CCGGTACATCATCTCCACCACCATCGCGCGCAAGAACCGCGAGCCCAAGCAGCATTA 227  
 Db |||||  
 QY 278 GTTACATGCTGAGCGGGTTGTTGNAACAGGTTTCTTCCGGATTTGTTTTCAGGCGAAT 337  
 Db |||||  
 QY 228 GCTACATGCGGCGCGGTTGTTGGGCACTGTTGCTGTTGGCATCGCTTTTCAGGCTAAAT 287  
 Db |||||

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QY 338 GCTTGGAACTGGAGAACTAGTAGCATTTAAAGGCTCTTGCAGATCGAGCTATAAAA 397
Db 288 GCCTGGAAACCGGGGAGATGGTGGCATTTAAGAGGTACTCGAGGACGAGCGTACAAGA 347
QY 398 ACCGTGAGTTGCAACTAATCGGACCAATGGATCCCAAAATGTCTCTCTTGAAGCACT 457
Db 348 ACCGTGAGTTGCAACTAATCGGATCGATGATCCCAAAATGTCTCTCTTGAAGCACT 407
QY 458 GTTCTTCTCTCAACAGAGTAGAGATGAGCTCTTCTCAACCTTGTATTGAGAGTAGTAC 517
Db 408 GCTTCTTCTCAACCAAGTAGAGATGAGCTCTTCTCAACCTTGTATTGAGAGTAGTAC 467
QY 518 CTGAGACTTTATACCGGCTTTGAGGCACTACTACTAGTCTTAATCAGAGGATGCCAATTT 577
Db 468 CGGAGACGCTATACCGGCTTTAAGGCACTACTAGTCTTAATCAGAGGATGCCAATTT 527
QY 578 TCTATGTCAAGCTTTATACATATCAATCTTTAGAGGTTTGGCTTACATCACTACTGTTTC 637
Db 528 TCTATGTCAAGCTTTATACATATCAAGCTTTTGGAGGCTAGCTTATGTTCACTGTTTC 587
QY 638 CGGTGTTTGGCACAGAGATGTGAACCAACCAAAATCTCTTGGTTGATCCCTTGAACCCATC 697
Db 588 CAGGAGTTTGGCACAGGATGTGAACCAACCAAAATGTTTGGTTGATCCCTTGAACCCATC 647
QY 698 AGTTAAGCTGTGATTTTGGAGTGTGAAGTATTTGGTCAAGGTGAACCAAAATATAT 757
Db 648 AAGTCAAGATCTGTGACTTTTGGAGTGTGAAGTATTTGGTCAAGGTGAACCAAAATAT 707
QY 758 CATATATCTGCTCCGCTTTATATCTGCTTCCAGAACTCATCTTTGGCGCCACAGAGTATA 817
Db 708 CATATATCTGCTCCGCTTTATATCTGCTTCCAGAACTCATCTTTGGCGCCACAGAGTATA 767
QY 818 CAGCATCCATAGATATATGCTGCTGTTGTGTAAGTCTGTCAGAGCTTCTTCTTGGCCAGC 877
Db 768 CAACCTTCAATAGATATATGCTGCTGTTGTGTAAGTCTGTCAGAGCTTCTTCTTGGCCAGC 827
QY 878 CGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGTTCTTGGTA 937
Db 828 CTCGTGTTCCAGGAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGTTCTTGGTA 887
QY 938 CTCCAACTCGTGAAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGTTCTTGGTA 997
Db 888 CTCCAACTCGTGAAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGTTCTTGGTA 947
QY 998 AAATCAAGCTCACCTTGGCAAGAGTTTTCATAAAGCGATGCTTCCAGAGCAATAG 1057
Db 948 AGATTAAGCTCATCTTGGCAAGAGTTTTCATAAAGCGATGCTTCCAGAGCAATAG 1007
QY 1058 ACCTTGCAATCTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGGGCTCGAAGCAT 1117
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QY 1118 GTGCTCATCGGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGGGCTCGAAGCAT 1177
Db 1068 GTGCTCATCGGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGGGCTCGAAGCAT 1127
QY 1178 CATTAACCGCAATGTTTCAATATTCACCAAGTCTAGCTGCACTGGGCTCGAAGCAT 1237
Db 1128 CATTAACCGCAATGTTTCAATATTCACCAAGTCTAGCTGCACTGGGCTCGAAGCAT 1187
QY 1238 ACAGGCTAATACCTGAGCATGTGAGACGCAAAATGAGCAC 1277
Db 1188 ACAGGCTAATACCTGAGCATGTGAGACGCAAAATGAGCAC 1227

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RESULT 3

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US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases

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; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
; US-09-854-731-15

Query Match      43.5%; Score 701.6; DB 4; Length 1673;
Best Local Similarity 74.7%; Pred. No. 3.5e-200;
Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 98 AGCCTCATGCTCTTGTCTCGCGCTGCGAGCTTCAAGCGGCGAGCGCTTTGAAACCGCCGTC 157
Db 48 AGCATCCGCGCGCGCGCGCGCGCGATGCTGCTCGAGCAGCAGCGCCCGCCACCGCAGTCG 107
QY 158 CTGAATGGATCTTGATTAAGAAATGCTGCGAGCTGTTATTGAGGGAATGACGCTGTTA 217
Db 108 CTTGCGAAGAAGCAGCAGGATGCGGAGCGCGCTATGCGAGGGGGAACGACGCCATGA 167
QY 218 CTGCTCATATCATTTCCACTACTATAGGAGCAAAACCGGCAACCAAGCAGACCATTA 277
Db 168 CCGTCACTCATCTCCACACCATCGCGCGCAAGAGCGGCGGCGCCCAAGCAGCATTA 227
QY 278 GTTACATGGCTGAGCGGCTTCTTGAACAGGTTCAATCGGGAATGTTTTTTCAGGCGAAAT 337
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QY 338 GCTTGGAAACTGGAGATCATAGTGCATTAATAAGGCTTTCGAGAGTCAAGCTATATAAA 397
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QY 398 ACCGTGAGTTGCAACTAATCGGACCAATGGATCACCACAAATGTCTATCTCTTGAAGCACT 457
Db 348 ACCGTGAGTTGCAACTAATCGGATGCTGATGATCCATTCATGTTGTTCTCTTCAAGCACT 407
QY 458 GTTCTTCTCTCAACAGAGTAGAGTGTCTTCTCAACCTTGTATTGAGAGTAGTAC 517
Db 408 GCTTCTTCTCAACCAAGTAGAGTGTCTTCTCAACCTTGTATTGAGAGTAGTAC 467
QY 518 CTGAGACTTTATACCGGCTTTGAGGCACTACTACTAGTCTTAATCAGAGGATGCCAATTT 577
Db 468 CGGAGACGCTATACCGGCTTTAAGGCACTACTAGTCTTAATCAGAGGATGCCAATTT 527
QY 578 TCTATGCAAGCTTTTACACATATCAAAATCTTTAGAGGTTTGGCTTACATCACTACTGTTTC 637
Db 528 TCTATGCAAGCTTTTACACATATCAAGCTTTTGGAGGCTAGCTTATGTTCACTGTTTC 587
QY 638 CCGGTGTTTGGCACAGAGATGTGAACCAACCAAAATCTCTTGGTTGATCCCTTGAACCCATC 697
Db 588 CAGGAGTTTGGCACAGGATGTGAACCAACCAAAATGTTTGGTTGATCCCTTGAACCCATC 647
QY 698 AGTTAAGCTGTGATTTTGGAGTGTGAAGTATTTGGTCAAGGTGAACCAAAATATAT 757
Db 648 AAGTCAAGATCTGTGACTTTTGGAGTGTGAAGTATTTGGTCAAGGTGAACCAAAATATAT 707
QY 758 CATATATCTGCTCCGCTTTATATCTGCTTCCAGAACTCATCTTTGGCGCCACAGAGTATA 817
Db 708 CATATATCTGCTCCGCTTTATATCTGCTTCCAGAACTCATCTTTGGCGCCACAGAGTATA 767
QY 818 CAGCATCCATAGATATATGCTGCTGTTGTGTAAGTCTGTCAGAGCTTCTTCTTGGCCAGC 877
Db 768 CAACCTTCAATAGATATATGCTGCTGTTGTGTAAGTCTGTCAGAGCTTCTTCTTGGCCAGC 827
QY 878 CGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGAGATCATATAAGTTCTTGGTA 937

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Db 828 CTCTGTTCCAGGAGAGACTGCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGGTA 887  
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Db 888 CTCCTCACTCGTGAAGAAATTCGATGATGAACCCGAACTACACAGATTTAGTTCCCAAC 947  
QY 998 AAATCAAGCTCACCCCTCGGCAAGGTTTTCATAAAGGATGCTCCAGAGCAATAG 1057  
Db 948 AGATTAAGGCTCATCTCTGGCAAGATTTTCCAAAGAGATGCGCGTGAAGCTATAG 1007  
QY 1058 ACCTTGCACTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCATCGGCTCGAAGCAT 1117  
Db 1008 ATCTTGCTCCCGCTTCTCCAGTATTCACCAATCTACGTTGCACGCTCTTGATGCAT 1067  
QY 1118 GTGCTCATCGGTTTTCATGAAGTCTCGAGAGCGCAACCGCGTCTTCCAAATGTCGTC 1177  
Db 1068 GTGCAATCTCTTCTTGTAGTACGTTGAGCGCAATGCGCTTGCAGAAATGCGCGC 1127  
QY 1178 CATTAACCGCATTTGTTCAATTTCAAAAGAGTTAGGTGGAGCTTCAATGGAGCTAATCA 1237  
Db 1128 CATTCCTCTCTGTTCACTTCAAACTGAACTAGCGAAGCGCTCTCCAGAGCTCATCA 1187  
QY 1238 ACAGGCTAATCTGAGCTGTGAGACGCAAAATGAGCAC 1277  
Db 1188 ACAGGCTTGTTCGGAACATGTTTCGACGCGCAAAATGGCCC 1227

## RESULT 4

US-09-347-801-9  
; Sequence 9, Application US/09347801  
; Patent No. 6262345

## GENERAL INFORMATION:

; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,438  
; EARLIER FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 1814  
; TYPE: DNA  
; ORGANISM: Zea mays

## US-09-347-801-9

Query Match 34.1%; Score 549.8; DB 3; Length 1814;  
Best Local Similarity 70.8%; Pred. No. 1.6e-154;  
Matches 731; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

QY 172 GATAAGAAATGCTCAGCTGTTATGAGGGAATGACGCTGTATCTGTCATATCAT 231  
Db 342 GACAGGACGTTGAAGATATGTTAGTCAATGGCAATGGGCGGAGCCTGGTCAATACATA 401  
QY 232 TCACACTACTAGGAGCAAAACGGGAACCAAGCAGACCAATTTAGTTACATGGCTGAG 291  
Db 402 GTGACGAGCATTTGATGGGAAATGGCGAGGCAAGCAGACCAATTTAGTTACATGGCTGAG 461  
QY 292 CGGTTGTTGGAACAGCTTCATTCGGGATGTTTTCAGCGGAAATGCTTGGAAATCGGA 351  
Db 462 CGGTTGTTGGAACAGCTTCATTCGGGATGTTTTCAGCGGAAATGCTTGGAAATCGGT 521  
QY 352 GAATCAGTACCAATTAAGGCTTTCGCAAGTACGAGTCAAGGCTTATTAAGGCTTTCGCA 411  
Db 522 GAGACGCTAGCTATAAGGCTTCTCAAGACAGAGATACAGAAATCGTGAAGTCA 581  
QY 412 CTAAATGGACCAATGATCAACCAATGCTATCTCTTGAAGCAGCTTCTCTCTACA 471  
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QY 472 ACGGTAGAGATGAGCTCTTCTCAACCTGTTATGAGGATATGATACCTGAGACTTTATAC 531  
Db 642 ACTGAGAAGAGAGGCTTTACCTCAATTTGGTGCTTGAGTATGATCCGAGACTGCTCAT 701  
QY 532 CGGGTTTGGAGCACTATCTAGTCTTAATCAGAGATGCGCAATTTTCTATGTCAGCTT 591  
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QY 592 TACACATATCAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGCTGTTGCCAC 651  
Db 762 TATATGTATCAGATTTGTAGAGCTTTGGCATACATTCACACAGCATTTGGAGTGGCCAC 821  
QY 652 AGAGATGTGAACACCAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTTAAGCTGTG 711  
Db 822 AGGACATTTAAGCCGCAAAATCTCTGGTTAATCTCATACCATCAGCTAAATTTGTG 881  
QY 712 GATTTTGAAGTGCAGAAAGTATTTGTCAAAGTGGAACCAACATATCATATATCTGCTCC 771  
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QY 892 GAAATTTCAAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAA 951  
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QY 1072 CTTCTTCAATATTCACCAAGTCTAGCTGCATCGGCTCGAAGCATGTGCTCATCGGTT 1131  
Db 1242 CTTCTGAGTACTCACCAAACTTCCGTCGACTGCTTTTGGAAAGCATTTGGTCCATCGGTT 1301  
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QY 1192 TTCAATTTTCAAAAC 1204  
Db 1362 TTCAATTTTAAAGC 1374

## RESULT 5

US-09-854-731-9  
; Sequence 9, Application US/09854731  
; Patent No. 6794561  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 9  
; LENGTH: 1814  
; TYPE: DNA  
; ORGANISM: Zea mays

## US-09-854-731-9

Query Match 34.1%; Score 549.8; DB 4; Length 1814;  
 Best Local Similarity 70.8%; Pred. No. 1.6e-154;  
 Matches 731; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

QY 172 GATAAGGAATGCTGAGCTGTTATGAGGGAATGAGCTGTGTACTGGTCATATCAT 231  
 DB 342 GACAAGAGCTTGAAGATATGTTAGTCAATGCAATGGGCGGAGCTGGTCATATCAT 401  
 QY 232 TCCACTACTATAGGAGGCAAAACCGGCAACCAAGCAGACCATATTAGTTACATGCTGAG 291  
 DB 402 GTGACGACCATTTGATGGGAGAAATGGGAGGCAAGCAGACCATTTAGTTACATGCTGAG 461  
 QY 292 CGGGTGTGGAAAGCTTCAATCGGATGTTTTCAGGCGAAATGCTTGGAAACTGGA 351  
 DB 462 CGGGTGTGGAGTCAATCGGCTTTCGGAACCGTTTTCAGGCGCAAGTGTCTTGGAACTGGT 521  
 QY 352 GAATCAGTAGCTATTAAGAGGCTTTCGAAGATCGAGCTATTAAGAAACCGTGAGTTGCA 411  
 DB 522 GAGACGCTAGCTATTAAGAGGCTTTCGAAGATCGAGCTATTAAGAAACCGTGAGTTGCA 581  
 QY 412 CTAATGCGACCAATGATCAACCAATGTCTCTTGAAGCACTGTTTCTCTCTACA 471  
 DB 582 ACCATGCGAGTCTTGACCAACCAATGTGTGGCTCTAAGCACTGTTTCTCTCTACA 641  
 QY 472 ACGAGTAGAGTACTCTTCTCAACCTTGTATGAGATGATGACCTGAGACTTTATAC 531  
 DB 642 ACTGAGAAAGAGGAGCTTTACCTCAATTTGGTGTGATGATGATGATGATGATGATGAT 701  
 QY 532 CGGGTGTGGAGCACTACTACTAGTTCTAATCAGAGGATGCGCAATTTCTATGTCAGCTT 591  
 DB 702 CGTGTCTCAAAACATTAACAAAGATGAACCGAGCGATGCTTGAATTTATGCAAACTG 761  
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 QY 652 AGAGATGTGAACCAACCAATCTTTGGTGTGATCCCTTGACCATCAGGTTAAGCTGTGT 711  
 DB 822 AGGACATTAAGCGCGCAAAATCTCTGGTTAATCTCTATACCATCAGCTAAATTTGTGT 881  
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 DB 882 GACTTTGGAGCGCGCAAAATCTCTGGTTAATCTCTATACCATCAGCTAAATTTGTGT 941  
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 DB 1182 CCATGGCATAAGATATTCATAAAAGGATGCTGCTGAGCGGTAGATCTGTTCCCTGAG 1241  
 QY 1072 CTTCTTCAATATTCAGAGTCTAGCTGCACTGGCTGCGAGCATGTGCTCATCCGTTT 1131  
 DB 1242 CTTCTGCACTACTACCAAAATCTCGGTCGATGCTTTTGGAGCATTTGGTCCATCCGTTT 1301  
 QY 1132 TTTCAATGAACTCCGAGAGCAACCGCTCTTCCAAATGTCGTCATTTACCGCAATG 1191  
 DB 1302 TTTGATGAATCTCGGAGTCCAAACACCGCTTACCAGATGCTGTTTCTTCCGCTCTC 1361

QY 1192 TTCAATTTCAAAC 1204  
 DB 1362 TTCAATTTTAAGC 1374

RESULT 6  
 US-09-347-801-13  
 ; Sequence 13, Application US/09347801  
 ; Patent No. 6262345  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Allen, Steve  
 ; APPLICANT: Lee, Jian Ming  
 ; TITLE OF INVENTION: Plant Protein Kinases  
 ; FILE REFERENCE: BB-1171  
 ; CURRENT APPLICATION NUMBER: US/09/347,801  
 ; CURRENT FILING DATE: 1999-07-02  
 ; EARLIER APPLICATION NUMBER: 60/092,438  
 ; EARLIER FILING DATE: July 10, 1998  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 13  
 ; LENGTH: 1429  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1202)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1237)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1297)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1340)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1376)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1410)  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1416)  
 ; US-09-347-801-13

Query Match 32.4%; Score 523.4; DB 3; Length 1429;  
 Best Local Similarity 69.6%; Pred. No. 1.2e-146;  
 Matches 723; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 171 TGATAAGGAATGTCTGAGCTGTTATTGAGGAAATGACGCTGTGTACTGGTCATATCAT 230  
 DB 224 TGATAGAGAAATGGAGCCAGTTGTTGATGGCAACGGAACGGAGAGAGCATATCAT 283  
 QY 231 TCCACTACTATAGGAGGCAAAACCGGCAACCAAGCAGACCATATTAGTTACATGCTGGA 290  
 DB 284 TGTGACTACCATTTGGGGTGAATGTTGTCAGCCCAAGCAGACTATAAGCTACATGCGAGA 343  
 QY 291 CGGGTGTGGAGAGGTTTCATTCGGGATGTTTTCAGGCGAAATGCTTGGAAACTGG 350  
 DB 344 CGGTGTGTAGGGCATGGATCATTTGGAGTTGTCTTTCAGGCTAAGTGTCTTGGAAACCGG 403  
 QY 351 AGAATCAGTAGCCATTAAGAAAGGCTTTGCAAGATCGAGCTATTAAGAAACCGTGAGTTGCA 410  
 DB 404 TGAACGTGTGCTATCAAAAAGGTTCTTCAAGACAGAGGTACAGAACCGGAGACTGCA 463  
 QY 411 ACTAATGCGAAATGGATCACCCAAATGTCTCTCTTGAAGCACTGTTTCTTCTCTAC 470  
 DB 464 AACATGCGCTTCTTGACCAACCAAAATGTGTTGCTTTGAAGCACTGTTTCTTCTCAAC 523  
 QY 471 AACGAGTAGAGTAGCTCTCTCCACCTTGTATGAGATGTGATACCTGAGACTTTATA 530

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Db 524 CACTGAAAGGATGAACATATACCTTAATTTGGTTCTCGAATATGTTCTCTGAAACAGTTAA 583
QY 531 CCGGGTTTTGAGGCACTATAGTTCTTAATCAGAGATGCGCAATTTTCTATGTCAAGCT 590
Db 584 TCGGGTGATAAAACATATACAAAGTTTAAACCAAGGATGCCACTGATATATGTGAACCT 643
QY 591 TTACACATATCAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGCCA 650
Db 644 CTATACATACCAGATCTTTAGGCGGTTATCTTATATTCATCGTTGTTGGAGTCTGCCA 703
QY 651 CAGAGATGGAACCAACCAAAATCTCTTGGTGTATCCCTTGACCCCATCAGGTTAAGCTGTG 710
Db 704 TCGGGATATCAAGCCTCAAAATCTATTTGGTCAATCCACACACTCACGAGTTAAATATG 763
QY 711 TGATTTTGGAGTGCAAAAGTATTTGTTCAAAAGTGAAACCAACATATATATATCTGCTC 770
Db 764 TGACTTTGGAGTGCAAAAGTATTTGGTAAAGGCGAACCAATATATATATATATATGTT 823
QY 771 CGTTATTTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGA 830
Db 824 TAGATACATAGAGCACCTGAGCTCATATTTGGCGCAACTGATATATATATATATATG 883
QY 831 TATATGCTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 890
Db 884 CGTCTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 943
QY 891 AGAAATTCAGTTGATCAGCTTCTGAGATCATATTTGGCGCCACAGAGTATACAGCATCCAT 950
Db 944 TGAGAGTGGAGTTGATCAACTTGTGAGATCATCAAGGTTCTGGGCACTCCCAAGGGA 1003
QY 951 AGAAATTCAGTTGATGAAACCGCAACTACACAGATTTTAGGTTTCCCAAAATCAAGCTCA 1010
Db 1004 AGAGTTAAGTGCATGAAACCTTAATATACAGATTTAAATTTCCACAGTTAAAGACA 1063
QY 1011 CCCTTGGCAACAGGTTTTTCATAAACGATGCTCCAGAGCAATAGACCTTGCACTCTCG 1070
Db 1064 TCCATGGCACAGATCTTCATAGCGCATGCGCTCCAGAGGCTGTTGATTTGGTATCAAG 1123
QY 1071 GCTTCTTCAATATTCACCAAGTCTACGCTGACGCTCGAGCATGCTCATCCGTT 1130
Db 1124 ACTACTACAATATCCCTCACTTGGGTCGACAGTTTATAGATGCTTGGACGCACTT 1183
QY 1131 ---TTTCAATGAATCCGAGAGCAAAACGCGCTCTTCCAAATGGTGTGCTCAATACCGCC 1187
Db 1184 TCCTTTGGAGCAATTCGNGATCCAAATCTCTGCTTGCCAAATGGGCGATCCNTCCAA 1243
QY 1188 ATTGTTCAATTCACAA 1206
Db 1244 AACTATTAATTCAAACCA 1262

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RESULT 7

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US-09-854-731-13
; Sequence 13, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1202)

```

```

; NAME/KEY: unsure
; LOCATION: (1237)
; NAME/KEY: unsure
; LOCATION: (1297)
; NAME/KEY: unsure
; LOCATION: (1340)
; NAME/KEY: unsure
; LOCATION: (1376)
; NAME/KEY: unsure
; LOCATION: (1410)
; NAME/KEY: unsure
; LOCATION: (1416)
; US-09-854-731-13

Query Match      32.4%; Score 523.4; DB 4; Length 1429;
Best Local Similarity 69.6%; Pred. No. 1.2e-146;
Matches 723; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 171 TGATAAGGAAATGTCTGACAGCTGTTATTAGGGAATAGACGCTGTATTCTGGTCAATCAT 230
Db 224 TGATAGAGAAATGGAAAGCCACAGTTTGTGATGGCAACGGAACGGAGACAGGACATATCAT 283
QY 231 TTCCACTACTATAGAGAGGCAAAAACGGCGAAACCAAGAGCAGACATTAGTTACATGCTGA 290
Db 284 TGTGACTACCATTTGGGGGTAGAAATGTTGTCAGCCCAAGCAGACTATAAGCTACATATGCG 343
QY 291 GCGGGTTGTTGAAACAGAGTTTCATTCGGGATTCGTTTTCAGGCGAAATGCTTGGAAACTGG 350
Db 344 GCGTGTGTAGGCGCATGGATCATTTGGAGTTGTCTTCCAGGCTAAGTGTCTTGGAAACCGG 403
QY 351 AGAATCAGTGTAGCCATTTAAAAAGGCTTTGCAAGATCGACGCTATATAAAACCGTGAGTTGCA 410
Db 404 TGAACCTGTGGCTATCAAAAGGTTCTTCAAGACAGAGGTACAGAACCGGAGCTGCA 463
QY 411 ACTAATGCAACCAATGGATCACCCAAATGTCTCTCTTGAAGCACTGTTCTTCTCTAC 470
Db 464 AACAAATGCGCCTTCTTGACCCCAAAATGCTGCTTTGAAGCACTGTTCTTCTTCAAC 523
QY 471 AACGAGTACAGATGAGCTCTTCTCAACCTGTTATGAGAGTATGTACCTGAGACTTTATA 530
Db 524 CACTGAAAGGATGAACATATACCTTAATTTGGTTCTCGAATATGTTCTTGAACAGTTAA 583
QY 531 CCGGGTTTTGAGGCACTATATAGTTCTTAATCAGAGGATGCCAAATTTTCTATGTCAAGCT 590
Db 584 TCGGGTGATAAAACATTTACAAAGTTTAAACCAAGGATGCCACTGATATATGTGAACCT 643
QY 591 TTACACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGCCA 650
Db 644 CTATACATACCAGATCTTTAGGCGGTTATCTTATATTCATCGTTGTTTGGAGTCTGCCA 703
QY 651 CAGAGATGTGAACCAACCAAAATCTCTTGGTTGATCCCTTTGACCCATCAGGTTAAGCTGTG 710
Db 704 TCGGGATATCAAGCCTCAAAATCTATTTGGTCAATCCACACTCACAGGTTAAATATG 763
QY 711 TGATTTTGGAGTGCAAAAGTATTTGGTCAAGGTGAACCAACATATATATATCTGCTC 770
Db 764 TGACTTTGGAGTGCAAAAGTATTTGGTAAAGGCGAAACCAATATATATATATATATGTT 823
QY 771 CGTTATTTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGA 830
Db 824 TAGATACATAGAGCACCTGAGCTCATATTTGGCGCAACTGATATATATATATATATG 883
QY 831 TATATGCTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 890
Db 884 CGTCTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 943
QY 891 AGAAATTCAGTTGATCAGCTTCTGAGATCATATAAGGTTCTTGGTGTCTTCCAACTCGTGA 950
Db 944 TGAGAGTGGAGTTGATCAACTTGTGAGATCATCAAGGTTCTGGGCACTCCCAAGGGA 1003
QY 951 AGAAATTCAGTTGATGAAACCGCAACTACACAGATTTTAGGTTTCCCAAAATCAAGCTCA 1010
Db 1004 AGAGTTAAGTGCATGAAACCTTAATATACAGATTTAAATTTCCACAGTTAAAGACA 1063

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QY 1011 CCCTTGGCACAAGTTTTCATAAAGGATGCTCCAGAGCAATAGACCTTGCATCTCG 1070  
Db 1064 TCCATGGCACAAGATCTTCCATAAGCGATGCTCCAGAGGCTGTGATTTGGTATCAAG 1123  
QY 1071 GCTTCTCAATATTCCACAAGTCTAAGCTGCACTCGCTCGAAGCATGTGCTCATCCGTT 1130  
Db 1124 ACTACTACATCTCCCTTAACCTGCGGTGCAAGTTTATAGTGCCTTGGAGCGACCTTT 1183  
QY 1131 ---TTTCAATGAATCCGAGAGCCAAAGCCCGTCTTCCAAATGGTCTGTCATTAACGCC 1187  
Db 1184 TCCCTTGGAGCAATCCGNGATCCAAATCCTCGCTTGCCAAATGGCGCATCCTCCAAAC 1243  
QY 1188 ATTGTTCAATTTCAACAA 1206  
Db 1244 AACTATAATTAACAAACCA 1262

RESULT 8  
US-09-489-765A-3  
; Sequence 3, Application US/09489765A  
; Patent No. 6323029  
; GENERAL INFORMATION:  
; APPLICANT: Madeline M. Butler  
; APPLICANT: Robert McKay  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES  
; FILE REFERENCE: RTS-0124  
; CURRENT APPLICATION NUMBER: US/09/489,765A  
; CURRENT FILING DATE: 2000-01-19  
; NUMBER OF SEQ ID NOS: 85  
; SEQ ID NO 3  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (40)... (1302)  
US-09-489-765A-3

Query Match 23.9%; Score 385.2; DB 3; Length 1389;  
Best Local Similarity 65.5%; Pred. No. 4.4e-105;  
Matches 596; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 295 GTTGTGGAAACAGGTTTCATTCGGGATTTGTTTTCAGGCGAAATGCTTGGAAACTGGAGAA 354  
Db 220 GTGATTGGAAATGGATCAITTTGGTGTGTATATCAAGCCAACTTTGTGATTCAGAGAA 279  
QY 355 TCAGTAGCCATTAAAGAGTCTTGAAGATCGACGCTATAAAACCGTGAGTTGCAACTA 414  
Db 280 CTGGTCGCCATCAAGAAAGTATTGCGAGCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339  
QY 415 ATGCGACCAATGGATCCCAATGCTCATCTCTTGAAGCACTGTTTCTCTC---TACA 471  
Db 340 ATGAGAAAGTAGATCACTGTAAACATAGTCCGATTGCGTATTCTTCTTACTCCAGTGGT 399  
QY 472 ACGAGTAGAGATGAGCTCTTCTCAACCTGTTGATGGAGTAGTACCTCGAGACTTTATAC 531  
Db 400 GAGAGAAAGATGAGTCTATCTTAATCTGGTGTGAGTATGTTCCGGAACAGATATAC 459  
QY 532 CGGGTTTGGAGCATACTATAGTTCTAATCAGAGGATGCCAAATTTTCTATGTCAAGTTT 591  
Db 460 AGAGTTGCCAGACACTATAGTGCAGGCCAAACAGAGCGCTCCCTGTGATTATGTCAAGTTG 519  
QY 592 TACATATCAATCTTTAGAGTTTGGCTTACATCCATCTGTTCCCGGTGTTGGCCAC 651  
Db 520 TATATGTATCAGCTGTTCCGAGTTTTCCTATATATCCATTCCTTT---GGAATCTGCCAT 576  
QY 652 AGAGATGTGAACACCAAAATCTCTTGGTGTGATCTCTTGACCCATCAGGTTAAGCTGTGT 711  
Db 577 CGGATATTAACCCAGAACCTCTTGTGGATCCTGATCTGCTGTATTAATAACTCTGT 636

## RESULT 9

US-09-016-434-1414

; Sequence 1414, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

```

; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g529236
; US-09-016-434-1414

Query Match      23.9%; Score 385.2; DB 4; Length 1389;
Best Local Similarity 65.5%; Pred. No. 4.4e-105;
Matches 596; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

QY 295 GTTGTGGAAACAGGTTCAATTCGGGATGTTTTCAGCGGAAATGCTTGGAAACTGGAGAA 354
Db 220 GTGATTGGAAATGGATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCCAGGAA 279
QY 355 TCAGTAGCCATTAAAGGCTCTTGCAGATCGAGCTATATAAACCGTGAGTTGCAACTA 414
Db 280 CTGCTCGCCATCAAGAAAGATTTCAGGCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
QY 415 ATCGACCAATGATCACCCAAATGTCATCTCTTGAAGCACTGTTTCTTCTC---TACA 471
Db 340 ATGAGAAAGCTAGTCACTGTACATAGTCCGATTGGTTATTTCTTCTACTCCAGTGT 399
QY 472 ACAGTAGAGATGAGCTCTTCTTCAACCTGTTTATGGAGTAGTACTGAGACTTTTATAC 531
Db 400 GAGAAGAAGATGAGTCTATCTTAATCTGCTGCTGACTATGTTCCGGAAACAGTATAC 459
QY 532 CGGTTTTGAGGCACATATAGTCTTCTAATCAGAGATCCCAATTTTCTATGTCAGCTT 591
Db 460 AGAGTTGCCCAACACTATAGTCAGGCAACAGCGCTCCCTGTGATTTATGTCAAGTTG 519
QY 592 TACACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATAGTCTTCCCGTGTTCGCCAC 651
Db 520 TATATGATCAGCTGTTCCGAAGTTTAGCTATATCCATCTCTT---GGAATCTCCAT 576
QY 652 AGAGATGTGAAACACAAATCTCTTGGTGTGTTGCTTGAACCATCAGGTTAAGCTGTGT 711
Db 577 CGGGATATTAAACCGCAGAACCTCTTGTGGATCTCTGATCTGCTGTATTAAACTCTGT 636
QY 712 GATTTTGGAGTCCAAAGATTGTTCAAGGTGAACCAACATATATATCTCTCTC 771
Db 637 GACTTTTGGAAAGTCAAGACGCTGGTCCGAGGAGAACCCAAATGTTTCGTATATCTGTCT 696
QY 772 CGTTATTATCGTCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCATCCATAGAT 831
Db 697 CGGTACTATAGGCAACAGAGTTGATCTTTGGAGCCACTGATTTATACCTTAGTATAGAT 756
QY 832 ATATGCTCTCGTGTGTGTAATCTTGGCAGAGCTTCTTCTTGGCCAGCGGTTATTTCCAGGA 891
Db 757 GTATGGTCTCTGCTGTGTGTGGTGTGCTGTAGCTGTGTACTAGGCAACCAATATTTCAGGG 816
QY 892 GAAATTCAGTTTCACTAGCTTGGAGATCATAAAGTTCTTGGTACTCCAATCTGTGA 951
Db 817 GATAGTGGTGTGATCAGTTGGTAGAAATTAATCAAGGTCCTGGAACTCCAAAGGGAG 876
QY 952 GAAATTCGATGTATGAACCCGAACTACACAGATTTTATAGTTTCCCAAAATCAAAGCTCAC 1011
Db 877 CAATCAGAGAAATGAACCAACTACACAGATTTTAAATTCCTCAATTAAGGCACAT 936
QY 1012 CTTTGGCAAGGTTTTTCAAAACGATGCTTCAGAGCCCTTCAAGCAATAGACCTTGCATCTCGG 1071
Db 937 CTTTGGCAATAGTCTTCCGACCCCGAACTCCACCGGAGGCAATTTGCACTGTGTAGCCGT 996
QY 1072 CTTCTTCAATATTACCAAGTCTACGCTGCACTGCGCTCGAAGCAATGCTCATCCGTTT 1131
Db 997 CTGCTGGAGTATACCAACACTGCCCGGACTAACACCTGGAAGCTGTGTGCAATTCATTT 1056
QY 1132 TTCAATGAATCCGAGAGCAAAACGCCCGCTTTTCCAAATGGTCTGCTCCATTTACCGCCATTG 1191

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RESULT 10
US-08-602-264A-1
; Sequence 1, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: february 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-08-602-264A-1

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Query Match      23.8%; Score 384.4; DB 2; Length 2088;
Best Local Similarity 65.6%; Pred. No. 9.8e-105;
Matches 594; Conservative 0; Mismatches 306; Indels 6; Gaps 2;

QY 299 TTGGAACAGGTTCAATTCGGGATGTTTTCAGCGGAAATGCTTGGAAACTGGAGAAATCAG 358
Db 800 TTGGAATCGATCAATTTGGTGTGTATATCAAGCCAAACTTTGTGATTCAGGAGAACTGG 859
QY 359 TAGCCATTTAAAGGTCCTTGGCAAGATCGAGCTATATAAACCGTGTGAGTTGCAACTAATGC 418
Db 860 TCGCCATCAAGAAAGTATTTCAGGCAAGAGATTTAAGAAATCGAGAGCTCCAGATCATGA 919
QY 419 GACCAATGATCACCCAAATGTCATCTCTTGAAGCACTGTTTCTTCTC---TACAACGA 475
Db 920 GAAAGTAGATCACTGTAAACATAGTCCGATTCGGTTATTTCTTCTACTCCAGTGGTGA 979
QY 476 GTAGAGATGAGCTCTTCTCAACCTTGTGTTATGGAGTATGTACTGAGACTTTTATACCGGG 535

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Db 980 AGAAGATGAGTCTATCTTAATCTGGTCTGGACTATGTTCCGGAACAGTATACAGAG 1039
Qy 536 TTTTGAGGACATATAGTCTTAATCAGAGGATGCCAATTTTCTATGTCAGCTTTTACA 595
Db 1040 TTGCCAGACATATAGTCGAGCAACAGACGCTCCCTGTGATTTATGTCAGAGTTGATA 1099
Qy 596 CATATCAATCTTTAGAGTTTGGCTTACATCATCTGTTCCCGGTGTTGCCACAGAG 655
Db 1100 TGTATCAGCTGTTCGGAAGTTTAGCCTATATCCATTCCTTT---GGAATCTGCCATCGG 1156
Qy 656 ATGTGAACACCAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTAAAGCTGTGTGATT 715
Db 1157 ATATTAAACCGCAGAACCTCTTGTGGATCTTGATCTGCTATATAAACHCTGTGACT 1216
Qy 716 TTGGAAGTGCAGAAAGTATTTGGTCAAGGTGAACCAACATATCATATATCTGCTCCGTT 775
Db 1217 TTGGAAGTGCAGAAAGTATTTGGTCCGAGGAGAACCAATTTTGGTATATCTGTTCTCGT 1276
Qy 776 ATATCTGCTCCAGACATCTCTTTGGGCGCACAGAGTATACAGATCATACATATATAT 835
Db 1277 ACTATAGGCGACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGAT 1336
Qy 836 GGTCTGCTGGTGTGTACTGTCAGAGCTCTCTTGGCCAGCGGTTATTTCCAGAGAAA 895
Db 1337 GGTCTGCTGGTGTGTGTGGCTGAGCTGTACTAGGACCAATATTTCCAGGGGATA 1396
Qy 896 ATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTTGGTACTCCAACTCCGTGAAGAAA 955
Db 1397 GTGGTGTGATCAGTTGGTGAAGTAAATCAAGTCTCGGAATCTCAACAGGGAGCAA 1456
Qy 956 TTCGATGTATGAACCGCAACTACAGATTTTAGTTTCCCAAAATCAAGCTCACCTT 1015
Db 1457 TCAGAGAAATGAACCAAACTACAGATTTTAAATTTCCCTCAAAATTAAGGCACATCCTT 1516
Qy 1016 GGCACAAGGTTTTTCATAAACGGATGCTTCCAGAGCAATAGACCTTGCATCTCGGCTTC 1075
Db 1517 GGACTAAGTCTTCCGACCCGAACTCCACCGGAGCAATTCGACTGTGTAGCCGTCTGC 1576
Qy 1076 TTCAATATTTCCAAAGTCTACGCTGACCTGCGCTCGAAGCATGTGCTCATCGTTTTTCA 1135
Db 1577 TGGAGTATACCAACTGCCGCACTAACACCACTGGAAGCTTGTGACATTCATTTTGTG 1636
Qy 1136 ATGAATCCGAGAGCAAAAGCCGCTTTCCAAATGGTGTGTCATACCGCAATTTGTCA 1195
Db 1637 ATGAATTCGAGGACCAAAATGTCAAACCTACCAATGGGCGAGACACACCTGCATCTTCA 1696
Qy 1196 ATTTCAT 1201
Db 1697 ACTTCA 1702

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RESULT 11  
US-08-461-018A-1  
; Sequence 1, Application US/08461018A  
; Patent No. 6071694  
; GENERAL INFORMATION:  
; APPLICANT: AKIHiko TAKASHIMA et al.  
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: WENDEROTH, LIND & PONACK  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; COUNTRY: D.C.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch,  
; MEDIUM TYPE: 1.44 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1

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; CURRENT APPLICATION DATA:  

; APPLICATION NUMBER: US/08/461.018A  

; FILING DATE: June 5, 1995  

; CLASSIFICATION: 514  

; PRIOR APPLICATION DATA:  

; APPLICATION NUMBER: 08/204,091  

; FILING DATE: March 2, 1994  

; ATTORNEY/AGENT INFORMATION:  

; NAME: Warren M. Cheek, Jr.  

; REGISTRATION NUMBER: 33,367  

; REFERENCE/DOCKET NUMBER:  

; TELECOMMUNICATION INFORMATION:  

; TELEPHONE:  

; TELEFAX:  

; TELEX:  

; INFORMATION FOR SEQ ID NO: 1:  

; SEQUENCE CHARACTERISTICS:  

; LENGTH: 2088 base pairs  

; TYPE: nucleic acid  

; STRANDEDNESS: double  

; TOPOLOGY: linear  

; MOLECULE TYPE: cDNA to genomic RNA  

; ORIGINAL SOURCE:  

; ORGANISM: human being  

; US-08-461-018A-1  

Query Match 23.8%; Score 384.4; DB 3; Length 2088;  

Best Local Similarity 65.6%; Pred. No. 9.8e-105;  

Matches 594; Conservative 0; Mismatches 306; Indels 6; Gaps 2;  

Qy 299 TTGNAACAGGTTTCATTCGGGATTTGTTTTCAGGCGAAATGCTTGGAAAAGTGGAGATCAG 358  

Db 800 TTGAAATGGATCATTTGGTGGTATATCAAGCCAAACTTTTGTGATTCAGGAGAACTGG 859  

Qy 359 TAGCCATTAAAAAGGCTTTGCAAGATCGACGCTATAAAAAACCGTCAGTTGCAACTAAATGC 418  

Db 860 TCGCATCAGAAAGTATTCGAGCAAGAGATTTAAGATCGAGAGCTCCAGATCATGA 919  

Qy 419 GACCAATGGATCACCAAAATGTCATCTCTTGAAGCACTGTTTCTTCTC---TACAACGA 475  

Db 920 GAAAGCTAGATCACTGTAAATAGTCGATTCGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 979  

Qy 476 GTAGAGATGAGCTCTTCTCAACCTTGTATGGAGTATGTACCTGAGACTTTTATACCGGG 535  

Db 980 AGAAGATGAGGCTCTATCTTAATCTGGTGTGAGTATGTTCCGGAACAGTATACAGAG 1039  

Qy 536 TTTTGAGGCACTATATAGTTCTTAATCAGAGGATGCCAAATTTTCTATGTCAAGCTTTTACA 595  

Db 1040 TTGCCAGACATATAGTCGAGCCAAACAGAGCTCCCTGTGATTTATGTCAGAGTTGATA 1099  

Qy 596 CATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGCCACAGAG 655  

Db 1100 TGTATCAGCTGTTCGGAAGTTTAGCCTATATCCATTCCTTT---GGAATCTGCCATCGG 1156  

Qy 656 ATGTGAACACCAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTAAAGCTGTGTGATT 715  

Db 1157 ATATTAAACCGCAGAACCTCTTGTGGATCTCTGATCTGCTGATTTATAAAGCTCTGTGACT 1216  

Qy 716 TTGGAAGTGCAGAAAGTATTTGGTCAAGGTGAACCAACATATCATATATCTGCTCCGTT 775  

Db 1217 TTGGAAGTGCAGAAAGTATTTGGTCCGAGGAGAACCAATTTTCCAGGGGATA 1276  

Qy 776 ATATCTGCTCCAGACATCTCTTGGGCGCACAGAGTATACAGATCATACATATATATAT 835  

Db 1277 ACTATAGGCGACAGAGTTGATCTTTGGAGCCACTGATTTATACCTCTAGTATAGATGAT 1336  

Qy 836 GGTCTGCTGGTGTGATCTGCGAGAGCTTCTTCTTGGCCAGCCGTTTATTTCCAGAGAAA 895  

Db 1337 GGTCTGCTGGTGTGATCTGCGAGAGCTTCTTCTTGGCCAGCCGTTTATTTCCAGGGGATA 1396  

Qy 896 ATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTTGGTACTCCAACTCCGTGAAGAAA 955  

Db 1397 GTGGTGTGATCAGTTGGTGAAGTAAATCAAGTCTCGGAATCTCAACAGGGAGCAA 1456

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QY 956 TTGATGATGAAACCGGAACTACACAGATTTTAGTTCCACAAATCAAAGCTCACCCCTT 1015  
 DB 1457 TCAGAGAAATGAACCCAACTACAGAAATTTAAATTCCTCAATTAAGGCACATCCTT 1516  
 QY 1016 GGCACAAGGTTTTTCATAAAGCGATGCCCTCCAGAACAAATAGACCTTGCATCTCGGCTTC 1075  
 DB 1517 GGACTAAGGCTTCCGACCCGAACTCCACCGGAGCAATTCACCTGTGTAGCCGCTGC 1576  
 QY 1076 TTCAATATTCACCAAGCTACGCTGCACCTGCGCTCGAAGCATGTGCTCATCGTTTTTCA 1135  
 DB 1577 TGAGATATACACCAACTGCCCGGACTAACCACTGGAAGCTTGTGCACATTCATTTTTTG 1636  
 QY 1136 ATGAATCCGAGAGCAAAAGCGCGCTTCCAAATGGTCCATTAACCGCAATTTGTTCA 1195  
 DB 1637 ATGAATTCGGAGACCAATGTCAAACTACCAATGGGAGACACACCTGCACCTTTCA 1696  
 QY 1196 ATTCA 1201  
 DB 1697 ACTTCA 1702

RESULT 12  
 US-09-216-958-1  
 ; Sequence 1, Application US/09216958  
 ; Patent No. 6248559  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akihiko TAKASHIMA et al.  
 ; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: WENDEROTH, LIND & PONACK  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; COUNTRY: D.C.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch,  
 ; MEDIUM TYPE: 1.44 mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/216,958  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/461,018  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; REFERENCE/DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE:  
 ; TELEFAX:  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2088 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to genomic RNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: human being  
 ; US-09-216-958-1

Query Match 23.8%; Score 384.4; DB 3; Length 2088;  
 Best Local Similarity 65.6%; Pred. No. 9.8e-105;  
 Matches 594; Conservative 0; Mismatches 306; Indels 6; Gaps 2;

QY 299 TTGGAACAGGTTCAITTCGGGATTTGTTTTTCAGCGAAATGCTTGGAACTGGAGATCAG 358  
 DB 800 TTGGAATGATCAITTTGGTGGTATATCAAGCCAACTTTGTGATTTCAGGAACTGG 859  
 QY 359 TAGCCATTTAAAGGCTTTGCAAGATCGACGCTATAAAACCGTGAGTTGCAACTTAATGC 418  
 DB 860 TCGCCATCAAGAAAGTATTGCAAGCAAGAGATTTAAGAAATCGAGAGCTCCAGATCATGA 919  
 QY 419 GACCAATGGATCACCAATATGTCCTCTCTCAAGCACTGTTCTTCTC- -TACAACA 475  
 DB 920 GAAAGTAGATCACTGTACATAGTCCGATTGCGTTATTTCTTACTCCAGTGGTGA 979  
 QY 476 GTAGAGATGAGCTCTTCTCAACCTTTGTTATCGAGTATGTACTCTGAGACTTTATACCGG 535  
 DB 980 AGAAGATGAGCTCTATCTTAATCTGGTCTGACTATGTTCCGGAAACAGTATACAGAG 1039  
 QY 536 TTTTGAGGCACTATATCTAGTTCTTAATCGAGAGATGCCAAATTTTCTATGTCAAGCTTTTACA 595  
 DB 1040 TTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAAGTTGTATA 1099  
 QY 596 CATATCAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGTGTTTGCACAGAG 655  
 DB 1100 TGTATCAGCTGTTCCGAAGTTTAGCTATATCAATTCCTTT- -GGAATCTGCCATCGG 1156  
 QY 656 ATGTGAACCAACAAATCTCTTGGTTGATCCCTTGACCCATCAGGTAAAGCTGTGTGATT 715  
 DB 1157 ATATTAAACCGCAGAACCTCTTGTGGATCTCTGATCTGCTGTTATAAATCTGTGACT 1216  
 QY 716 TTGGAAGTGCAAAAGTATTGGTCAAAGGTGAACCAAAACATATCATATATCTGCTCCGTT 775  
 DB 1217 TTGGAAGTGCAAAAGCAGCTGGTCCGAGGAGAAACCAATTTCTGATATCTGTCTCGGT 1276  
 QY 776 ATTATCGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATAT 835  
 DB 1277 ACTATAGGCACACAGAGTTGATCTTTGGAGCCACTGATTTATACCTTAGTAGATGAT 1336  
 QY 836 GGTCTGCTGTTGTGTACTGGCAGAGCTTCTTTCTTGGCCAGCGCTTTATTTCCAGGAGAAA 895  
 DB 1337 GGTCTGCTGCTGTGTGTGGCTGAGCTGTACTAGGACAACCAATATTTCCAGGGGATA 1396  
 QY 896 ATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTGGTACTCCAACCTCGTGAAGAAA 955  
 DB 1397 GTGGTGTGGATCAGTTGGTAGAAATAATCAAGGTCCTGGGAACTCCAAACAAGGGAGCAA 1456  
 QY 956 TTTCGATGTATGAACCGCACTACACAGATTTTAGGTTCCCAAAATCAAAGCTCACCCCTT 1015  
 DB 1457 TCAGAGAAATGAACCCAACTACAGAAATTTAAATTTCCCTCAATTAAGGCACATCCTT 1516  
 QY 1016 GGCACAAGGTTTTTTCATAACGGATGCCCTCCAGAGCAATAGACCTTGCATCTCGGCTTC 1075  
 DB 1517 GGACTAAGGCTTTCGACCCCGAACTCCACCGGAGGCAATTCACCTGTGTAGCCGCTGC 1576  
 QY 1076 TTCAATATTCACCAAGCTTACGCTGCATCGCGTGAAGCATGTGCTCATCGTTTTTCA 1135  
 DB 1577 TGGAGTATACACCAACTGCCCGCACTAAACACCACTGGAAGCTTGTGCACATTCATTTTTTG 1636  
 QY 1136 ATGAACTCCGAGAGCCAAAGCGCGCTTTCAAAATGGTCCATTTACCGCAATCTGTCA 1195  
 DB 1637 ATGAATTACGGGACCCAAATGTCAAACTACCAATGGGCGAGACACACCTGCACCTTTCA 1696  
 QY 1196 ATTCA 1201  
 DB 1697 ACTTCA 1702

RESULT 13  
 US-09-566-921-24  
 ; Sequence 24, Application US/09566921  
 ; Patent No. 6682888  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loring, Jeanne F.  
 ; APPLICANT: Tingley, Debora W.  
 ; APPLICANT: Edwards, Carla M.

; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

; FILE REFERENCE: PA-0024 US

; CURRENT APPLICATION NUMBER: US/09/566,921

; CURRENT FILING DATE: 2000-05-05

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PERL Program

; SEQ ID NO 24

; LENGTH: 1952

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6582888 234735.15

US-09-566-921-24

Query Match

Best Local Similarity 23.3%; Score 375.8; DB 4; Length 1952;

Matches 637; Conservative 0; Mismatches 392; Indels 6; Gaps 2;

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QY 246 AGGCAAAACGGCGCAACCAAGCAGACCATTTAGTGTGAGCGGGTGTGGGAAC 305
DB 211 AGGCCAAGCCCGAGAGCGCTCCCAAGAAGTGGCTTACACGGACATCAAAAGTGATGGCAA 270
QY 306 AGGTTCAATTCGGGATTTGTTTTCAGCGGAATGCTTGGAACTGGAGATCAGTAGCCAT 365
DB 271 TGGCTCATTTGGGGTGGTGTACCGGACGCGCTGGCAGACACAGGGAAGTGTGCGCAT 330
QY 366 TAAAAAGGTTTGAAGATCGACGGCTATAAAACCGTGTGAGTGGCAACTAATCGCAACCAAT 425
DB 331 CAAGAAGGTTCTCAGGACAGAGGTTCAAGAACCGAGGCTGCAGATCATGCGTAAGCT 390
QY 426 GGATCACCACAAATGTCATCTCTTGAAGCAGCTGTTTCTTCTC---TACAAACGAGTAGAGA 482
DB 391 GGACCACTGCAATATTGTGAGGCTGAGATCTTTTCTACTCCAGTGGCGAGAAAGA 450
QY 483 TGAGCTTCTTCAACCTTGTATGGAGTATGTACTGTAGACTTTTATCCGGTGTGGAG 542
DB 451 CGAGCTTTACCTTAAATCTGGTGTGGAATATGTGCCGAGACAGTGTACCGGGTGGCCGG 510
QY 543 GCACATATACTAGTCTTAATCAGAGATGCCAATTTCTATGTCAAGCTTTACACATATCA 602
DB 511 CCACCTTACCAGGCGAAGTGTGACCATCCCTATCTCTATGTCAAGGTGTATCATGTACCA 570
QY 603 AATCTTTAGAGTTTGGCTTACATCATCTGTTCCCGGTGTTTCCACAGAGATGTGAA 662
DB 571 GCTCTTCGCGAGCTTGGCTTACATCACTC---CCAGGGCGTGTGTACCGGACATCAA 627
QY 663 ACCAATAATCTTGGTGTATCCCTTGACCATCAGGTTAAGCTGTGTGATTTTGGAG 722
DB 628 GCGCCAGAACCTGCTGGTGGACCTTGACACTGCTGTCTCAAGCTCTGCGATTTTGGCAG 687
QY 723 TGCAAAAGTATTGGTCAAGGTGAACCAACATATATATATCTGCTCCCGTTATTATCG 782
DB 688 TGCAAGCGTATTGGTCCGAGGGAGCCCAATGTCTTACATCTGTTCTCGCTACTACCG 747
QY 783 TGCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCATCCATAGATATATGCTGTC 842
DB 748 GSCCCCGAGAGCTCATCTTTGGAGCCACTGTATACACCTCATCCATCGATGTTTGTCTAGC 807
QY 843 TGGTGTGTATGGCAGAGCTTCTTCTTGGCCAGCGGTTATTTCCAGGAGAAATTCAGT 902
DB 808 TGGCTGTGTACTGGCAGAGCTCTCTTCTGGCCAGGCCCATCTTCCCTGGGGACAGTGGGGT 867
QY 903 TGATCAGCTTGGAGATCATAAAGTTCTTGGTACTCCAACTCGTGAAGAAATTCGATG 962
DB 868 GGACCAAGCTTGGGAGATCATCAAGGTGTCTGGAAACACCAACCCGGGACAAATCCGAGA 927
QY 963 TATGAACCCGAACACTACAGATTTTATAGTTTCCCAAAATCAAAGCTCAACCTTGGCACAA 1022
DB 928 GATGAACCCCAACTACACGAGTTCAAGTTCCCTCAGATTAAGCTCAACCTTGGACAA 987
QY 1023 GGTTTTTCATAAACCGATGCTTCCAGAGCAATAGACCTTGTGATCTCGGCTTCTTCAATA 1082
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DB 988 GGTGTTCAAATCTCGAACCGCGCCAGAGCCCATCGCGCTGTGCTCTAGCTCTCGAGTA 1047
QY 1083 TTCACCAAGTCTACGCTGCACCTCGCTCGAAGCATGTGCTCATCGGTTTTTCAATGAAC 1142
DB 1048 CACCCCATCTCAAGGCTCTCCCACTAGAGCGCTGTGGCAGACAGCTTCTTTGATGAAC 1107
QY 1143 CGAGAGCAAAACGCCGCTCTTCCAATGTTGTTGTTCCATTAACGGCATTTGTTCAATTC 1202
DB 1108 GCGATGTCTGGGAACCCAGCTGCTTAACAACCGCCCACTTCCCTCTCTTCAACTTCAG 1167
QY 1203 ACAAGAGTTAGTGGAGCTTCAATGGAGCTTAATCAACAGGCTAATACCTTGAGCATGTGAG 1262
DB 1168 TGCTGTGAATCTCTCCATCCACCGTCTCTCAAGCCATTTCTATCCCTCTCCTCACTTGAG 1227
QY 1263 ACACAAATGAGCAC 1277
DB 1228 GTCCCGAGCGGCAC 1242

RESULT 14
US-09-488-856A-3
; Sequence 3, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RTS-0115
; CURRENT APPLICATION NUMBER: US/09/488,856A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)...(1543)
US-09-488-856A-3

Query Match 23.3%; Score 375.8; DB 3; Length 2154;
Best Local Similarity 61.5%; Pred. No. 3.9e-102;
Matches 637; Conservative 0; Mismatches 392; Indels 6; Gaps 2;

QY 246 AGGCAAAACGGCGCAACCAAGCAGACCATTTAGTGTGAGCGGGTGTGGGAAC 305
DB 412 AGGCCAAGCCCGAGAGCGCTCCCAAGAAGTGGCTTACACGGACATCAAAAGTGTGGCAA 471
QY 306 AGGTTCAATTCGGGATTTGTTTTCAGCGGCAAAATGCTTGGAACTGGAGAACTAGTAGCCAT 365
DB 472 TGGCTCATTTGGGGTGGTGTACCGAGCAGCGCTGGCAGACACAGGGAACATAGTCGCCAT 531
QY 366 TAAAAAGTCTTGAAGATCGACGGCTATAAAACCGTGTGAGTTGCAACTAATCGGACCAAT 425
DB 532 CAAGAAGGTTCTCCAGGCAAGAGGTTCAAGAACCGAGAGCTGCAGATCATCGTAAAGCT 591
QY 426 GGATCACCACCAATGCTCTCTTGAAGCAGCTGTTTCTTCTC---TACAAACGAGTAGAGA 482
DB 592 GGACCACTGCAATATTGTGAGGCTGAGATATCTTTTCTACTCCAGTGGCGAGAAAGAGA 651
QY 483 TGAGCTTCTCTCAACCTTGTATGAGTATGTACTCGAGACTTTTATACCGGGTTTTGAG 542
DB 652 CGAGCTTTACCTTAATCTGGTGTGGAATATGTGCCGAGACAGTGTACCGGGTGGCCCG 711
QY 543 GCACATATACTAGTCTTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTACACATATCA 602
DB 712 CCACCTTCAACCAAGGCAAGTTGACCATCCCTATCTCTATGTCAAGGTGTATCATGTACCA 771
QY 603 AATCTTTAGAGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGGCCACAGAGATGTGAA 662
DB 772 GCTCTTCCGAGCTTGGCTTACATCCACTC---CCAGGGCGTGTGTCTACCGCGACATCAA 828
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QY 663 ACCACAAATCTCTGTTGATCCCTTGACCATCAGGTTAAGCTGTGTGATTTTGGAG 722
DB 829 GCCCAGAACCTGCTGTGGACCTGACACTGCTGTCTCAAGCTCTGGATTTGGCAG 888
QY 723 TGCAAAGATTGGTCAAAAGTGAACCAACATATCATATATCTGCTCCGTTATPATCG 782
DB 889 TGCNAAGCAGTTGGTCCGAGGGGAGCCCAATGCTCTCATCTGTCTCGCTACTACCG 948
QY 783 TGCTCAGAACTCATCTTTGGGCGCACAGATATACAGCATCATATATATGTCCTGC 842
DB 949 GGGCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCATCATCGATGTTGGTCAG 1008
QY 843 TGCTGTGTACTGGCAGAGCTCTCTTGCGCAGCGGTTATTTCAGGAGAAATTCAC 902
DB 1009 TGCTGTGTACTGGCAGAGCTCTCTTGCGCAGCGGTTATTTCAGGAGAAATTCAC 1068
QY 903 TGATCAGCTTGTGGAGATCAAAAGTTCTTGCTACTCCAACTCGTGAAGAAATTCGATG 962
DB 1069 GGACCAAGCTGGTGAGATCATCAAGTGTCTGGGAACACCAACCGGGAACAAATCCGAG 1128
QY 963 TATGAACCGAATACACAGATTTTAGTTTCCACAAATCAAGCTCACCTTGGCACAA 1022
DB 1129 GATGAACCGCAATACACAGAGTTCAAGTTCCCTCAGATTAAGCTCACCTTGGCAAA 1188
QY 1023 GGTGTTTTCATAACGATGCTCCAGAACCAATAGACCTTGCATCTCGGCTTCTTCAATA 1082
DB 1189 GGTGTTTTCATAACGATGCTCCAGAACCAATAGACCTTGCATCTCGGCTTCTTCAATA 1248
QY 1083 TACCAAGCTTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTTTTCATGAAT 1142
DB 1249 CACCCCATCTCAAGCTCTCCCACTAGAGGCTGTGCGCAGCTTCTTGAATGAAT 1308
QY 1143 CGAGAGCCAAAGCCGCTTCCAAATGGTGTGCTCAATACCGCATTTGTTCAATTTCAA 1202
DB 1309 GCGATGCTGCGAACCAGCTGCTTAAACACCGCCCACTTCCGCTTCTTCAACTTCAG 1368
QY 1203 ACAAGAGTTAGTGGAGCTTCAATGAGCTTAATCAACAGGCTAATACCTGAGCATGTAG 1262
DB 1369 TGTGTTGTAATCTCCATCAACCGCTCTCAACGCGCATCTCATCCCTCCTCACTTGA 1428
QY 1263 ACACAAATGAGCAC 1277
DB 1429 GTCCCGAGCGGCAC 1443

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RESULT 15
US-08-602-264A-2
; Sequence 2, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROOTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; US-08-602-264A-2

Query Match 23.2%; Score 373.8; DB 2; Length 1972;
Best Local Similarity 63.9%; Pred. No. 1.5e-101;
Matches 599; Conservative 0; Mismatches 332; Indels 6; Gaps 2;

QY 268 CAGACCATTTAGTTACATGCTGAGCGGTTGTTGGAAACAGGTTTCATTTCGGGATTTGTTTT 327
DB 293 CAGGAAGTCAGTTACAGACACTAAAGTCATTGGAAATGGGTTCATTTCGGTGTGATAT 352
QY 328 CAGGCGAAATGCTTGGAAACCTGGAGAACTCAGTAGCCATTAAAGAGTCTTTCGAAGTCGA 387
DB 353 CAAGCCAACTTTGTGACTCAGAGAACTGGTGGCCATCAAGAAAGTTCTTCAGGACAAG 412
QY 388 CGCTATAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCTCAATGTCATCTCC 447
DB 413 CGATTTAAGAACCGGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTCCGA 472
QY 448 TTGAAGACCTGTTTCTTCTC---TACAACGAGTAGAGATGAGCTTCTCCTCAACCTTGT 504
DB 473 TTGCGGTATTTCTTCTACTCGAGTGGCAGAGAAAGATGAGGTCTACCTTAACCTGGTG 532
QY 505 ATGGAGTAGTATACCTGAGACTTTTATACCGGGTTTGGAGCCTATATCTAGTTCTTAATCAG 564
DB 533 CTGGACTATGTTCCGGAAACAGTACAGAGTCGCCAGACACTATAGTCGAGCCAAGCAG 592
QY 565 AGGATGCCAATTTCTATGTCAAGCTTTTACACATATCAAAATCTTTAGAGAGTTGGCTTAC 624
DB 593 ACACCTCCCTGTGATCTATGTCAAGTTGTATATGTACCAGCTGTTCAGAAAGCTAGCCTAT 652
QY 625 ATCCATCTGTTCCCGGTTGTTGCCACAGAGATGTGAAACCCACAAAATCTCTTGGTTGAT 684
DB 653 ATCCATCTCCTTT---GGGATCTGCCATCGAGACATTTAAACCCACAGAACTCTTCTGGAT 709
QY 685 CCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGCAGAAAGTATTTGGTCAAAGGT 744
DB 710 CTTGATACAGCTGTATTAATACTCTGCGACTTTGGAAGTGCAGAGCAGCTGGTCCGAGGA 769
QY 745 GAACCAACATATCATATATCTGCTCCCGTTTATCTGCTGCTCCAGAACTCATCTTTGGC 804
DB 770 GAGCCCAATGTTTCATATATCTGTTCTCGGTACTACAGGGCCACAGAGCTGATCTTTGGA 829
QY 805 GCCACAGAGTATACAGCATCCATAGATATATGCTGCTGTTGTGTACTTGGCAGAGCTT 864
DB 830 GCCACCATTTACAGCTAGTATAGATGTATGTTCTGCGAGGCTGTGTGTTGGCTGATTTG 889
QY 865 CTTCTTGGCCAGCGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCAT 924
DB 890 TTGCTAGGACAAACCAATATTTCTGCGGACAGTGGTGTGATCAGTTGGTGGAAATAA 949
QY 925 AAGGTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTATGTAACCGGACTACAGAT 984
DB 950 AAGGTTCTTAGGAACACCAACAGGGGAGCAAAATTAGAGAAATGAACCCAAATTATACAGAA 1009

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Qy	985	TTTAGGTTCCCAAAATCAAGCTCACCTTGGCACAAGGTTTTCATAAACGGATGCCT	1044
Db	1010	TTCAAAATCCCCAAATCAAGGCACATCTTGGACGAAGGTTTCGGCCCCGAACTCCA	1069
Qy	1045	CCAGAAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTACCAAGTCTACGGTGCCT	1104
Db	1070	CCAGAGGCAATCGCACTGTGTAGCCGTCTCTGGAGTACACGCCGACCCCGGCTAACA	1129
Qy	1105	GGCTCGAAGCATGTGCTCATCGGTTTTTCAATGAATCCGAGAGCCAAACGCCGTCTTT	1164
Db	1130	CCACTGGAAGCTTGTGCACATTTTGTGATGAATTACGGGACCCAAATGTCAAACTA	1189
Qy	1165	CCAAATGGTCTCCATTACCGCCATTGTTCAATTCA	1201
Db	1190	CCAAATGGGCGAGACACACCTGCCCTCTTCAACTTTA	1226

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OM nucleic - nucleic search, using sw model

Run on: June.23, 2005, 10:41:47 ; Search time 1739.22 Seconds  
(without alignments)  
5800.480 Million cell updates/sec

Title: X99696  
Perfect score: 1614  
Sequence: 1 AGCAAGAGAGAGAGAAAA.....CCAAAAA.....1614

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10J\_PUBCOMB.seq.\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	972.2	60.2	1636	21	US-10-764-138-6
2	763.2	47.3	1744	16	US-10-292-408-25
3	713.2	44.2	1831	19	US-10-437-963-98579
4	710.4	44.0	1143	9	US-09-938-842A-875
5	710.4	44.0	1143	11	US-09-938-842A-875
6	710.4	44.0	1490	21	US-10-477-687-12
7	706.2	43.8	1726	18	US-10-425-114-12807

8	706.2	43.8	1979	18	US-10-424-599-67990
9	701.6	43.5	1673	9	US-09-854-731-15
10	699.8	43.4	1881	18	US-10-424-599-67987
11	699.2	43.3	1744	18	US-10-424-599-67989
12	698.2	43.3	2519	18	US-10-424-599-124786
13	693.4	43.0	1499	16	US-10-292-408-21
14	693.4	43.0	1553	18	US-10-424-599-26109
15	684	42.4	1779	20	US-10-425-115-22950
16	683	42.3	1922	19	US-10-437-963-29872
17	678.8	42.1	1621	16	US-10-292-408-15
18	676.8	41.9	1614	18	US-10-425-114-17458
19	676.8	41.9	1703	18	US-10-425-114-13850
20	676.8	41.9	1868	20	US-10-425-115-32308
21	673	41.7	1698	18	US-10-425-114-35222
22	669	41.4	1887	18	US-10-425-114-32993
23	665	41.2	1828	20	US-10-425-115-32310
24	659.2	40.8	1808	20	US-10-739-930-4849
25	657.4	40.7	1936	19	US-10-437-963-24168
26	645	40.0	2103	20	US-10-425-115-22953
27	621.8	38.5	1711	18	US-10-425-114-22299
28	620.2	38.4	1600	18	US-10-425-114-34808
29	620.2	38.4	1645	18	US-10-425-114-4124
30	618.6	38.3	1818	20	US-10-425-115-148434
31	585.6	36.3	1766	18	US-10-425-114-26106
32	585.6	36.3	1807	19	US-10-767-701-14202
33	582.8	36.1	1564	18	US-10-425-114-3272
34	582.8	36.1	1675	18	US-10-425-114-30667
35	581.2	36.0	1672	18	US-10-425-114-32862
36	579.6	35.9	2573	20	US-10-425-115-111277
37	573.8	35.6	2794	19	US-10-437-963-9995
38	571.2	35.4	1589	18	US-10-424-599-67975
39	571.2	35.4	1589	18	US-10-425-114-29569
40	571	35.4	1833	20	US-10-739-930-5123
41	567.6	35.2	1849	16	US-10-292-408-2
42	563	34.9	2165	19	US-10-437-963-24107
43	562.2	34.8	1635	18	US-10-425-114-9488
44	562.2	34.8	1867	18	US-10-424-599-81473
45	560.4	34.7	1817	18	US-10-425-114-8223

#### ALIGNMENTS

RESULT 1  
US-10-764-138-6  
; Sequence 6, Application US/10764138  
; Publication No. US20050081266A1  
; GENERAL INFORMATION:  
; APPLICANT: Sudwestdeutsche Saatzeucht-SWS  
; APPLICANT: Advanta Seeds B.V.  
; TITLE OF INVENTION: Modulation of Storage Organs  
; FILE REFERENCE: 026-1  
; CURRENT APPLICATION NUMBER: US/10/764,138  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: US/09/578,194  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; TYPE: DNA  
; LENGTH: 1636  
; ORGANISM: Arabidopsis sp.  
; FEATURE:  
; NAME/KEY: mRNA  
; LOCATION: (1)..(1636)  
; OTHER INFORMATION: strain Columbia ecotype  
; OTHER INFORMATION: taxon:3702  
; OTHER INFORMATION: tissue type leaves  
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots  
; PUBLICATION INFORMATION:  
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lechamny, A. and Kreis, M.  
; TITLE: Three New cDNAs Related to SG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)  
; TITLE: from Arabidopsis thaliana ( Accession No. X94938, x94939 and X99696) ( PGR97-

Instant  
Case

Query Match	60.2%;	Score 972.2;	DB 21;	Length 1636;
Best Local Similarity	77.0%;	Pred. No. 6.3e-260;		
Matches 1234;	Conservative	0;	Mismatches 343;	Indels 26;
Gaps	3;			
38	TTCCAGTGGTGTGAGAGAGAAAGAG-TAAATAAGACACATGGCTCATTAACCATTCGGGCGCT	96		
9	TTCCAGTGGAGAGAGAGTGTAGAGCTGTAAAGACACATGACTTCATTAACCATTCGGGCGCT	68		
97	CAGCCTCATGC-----TCTTCTCGCGCGCTTCAGAGCTTCACGAGCGGCGAGCTTTGAAA	150		
69	CCTCAGCCTCCGTCCTTAGCTCCTCAGCGCGCATCTTCACGGGGAGATCTTTGAAA	128		
151	CGCGCTCTGAATGTGATTAAGGAATGTCTGACGTGTGATTAAGGGGAAATGAC	210		
129	CGTCTCGCGATATACACACAGCAAGGAATGTCTGCTGTGTATAGAGGAAATGAT	188		
211	GCCTGTACTGTCATATCTTCCACTACTATAGGAGGCAAAACGGCGACCAAGCAG	270		
189	GCCTGTACCGGTACACATAATTTCTACTCAATTTGAGGCAAAATTTGGTGAACCTTAAACAG	248		
271	ACCATTTAGTTTACATGCTCAGCGGCTGTGTGAAACAGGTTCATTCGGGATTTGTTTTCAG	330		
249	ACCATTTAGTTTACATGCTCAGCGGCTGTGTGAAACAGGTTCATTCGGGATTTGTTTTCAG	308		
331	GCAGAAATGCTTGAACACTCGGAGAAATCAGTAGCCATTAAGAGTCTTTCAGAGATCGAGCG	390		
309	GCAGAAATGCTTGAACACTCGGAGAAATCAGTAGCCATTAAGAGTCTTTCAGAGATCGAGCG	368		
391	TATATAAACCGGTGAGTTCGAACTTAATGCGACCAATGATGATCCCAAAATGCTATCTCTTG	450		
369	TATATAAACCGGTGAGTTCGAACTTAATGCGACCAATGATGATCCCAAAATGCTATCTCTTG	428		
451	AAGCACTGTTCTTCTCTACACGAGTAGAGTAGCTCTTCTCAACCTTTGTTATGGAG	510		
429	AAGCACTGTTCTTCTCTACACGAGTAGAGTAGCTCTTCTCAACCTTTGTTATGGAG	488		
511	TATGTACCTGAGACTTTATACCGGGTTTGGAGCACTATCTAGTTCCTTAATCAGAGATG	570		
489	TATGTACCTGAGACTTTATACCGGGTTTGGAGCACTATCTAGTTCCTTAATCAGAGATG	548		
571	CCAAATTTCTATGCTCAAGCTTTACACATATCAAACTTTTAGAGGTTTGGCTTATCATCAT	630		
549	CCTATCTCTATGCTCAAACTTTACACATATCAAACTTTTAGAGGTTTGGCTTATCATCAT	608		
631	ACTGTTCCCGGCTTTTGCACAGAGATGTAACCAACCAAAATCTCTGTTGATCCCTTG	690		
609	ACTGTTCCCGGCTTTTGCACAGAGATGTAACCAACCAAAATCTCTGTTGATCCCTTG	668		
691	ACCCATCAGGTTAAGCTGTGTATTTTGAAGTGCAGAAAGTATTTGGTCAAAAGGTGAACCA	750		
669	ACCCATCAGGTTAAGCTGTGTATTTTGAAGTGCAGAAAGTATTTGGTCAAAAGGTGAACCA	728		
751	ACATATCATATATCTGCTCCGCTTTATATATGCTGCTCCAGAACTCATCTTTGGGCGCCACA	810		
729	ACATATCATATATCTGCTCCGCTTTATATATGCTGCTCCAGAACTCATCTTTGGGCGCCACA	788		
811	GAGTATACAGATCCATAGATATATGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	870		
789	GAGTATACATCATCCCAATGATATATGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	848		
871	GGCCAGCGGTTATTTCCAGGAGAGAAATTCAGTTTGTATGATGCTTTGTGGAGATCATAAAGTTT	930		



Query Match	47.3%	Score 763.2	DB 16	Length 1744
Best Local Similarity	78.6%	Match. No. 1.3e+201		
Matches	912	Conservative 0	Mismatches 248	Indels 0
Qy	115	CCGCGCTGCAGCTTCACGACGGCGACGCTTTGAAAACGCCGCTCCTGAATTGGATTCTGTAT	174	
Db	112			
Qy	175	AAGGAAATGTCTGCAGCTGTTATTAGAGGAAATGACGCTGTATTCTGGTCAATATCATTTTCC	234	
Db	172	AAGGATATGTCACTACTGTCTATTAGAGGGAATGATGCTGTCACTGGCCCAATATCTTCC	231	
Qy	235	ACTACTATPAGGAGCAAAAACGGCGAAACAAAGCAGACCATTAGTTATCATGCGCTGAGCGG	294	
Db	232	ACCACAAATTGGAGCAAAAATGGGGAACTTAAGAGACCATCAGTTTACATGCGCAGAACGT	291	
Qy	295	GTTGTTGGAACAGGTTCAATTCGGGATGTGTTTTTCAGGGGAAATGCTTGGAAACTTGGAGAA	354	
Db	292	GTTGTTGGCACTGGATCATTTTGGAGTTGTGTTTTTCAGGCAAAAGTCTTTGGAGACTTGGAGAA	351	
Qy	355	TCAGTAGCCATTAAAAAGGTCCTGCAGATCGACGCTATAAAAAACGGTAGGTGCGCACTA	414	
Db	352	GCAGTGGCTATTAAAAAGGTTCTTGCAGAAGGGCGGTACAAAAATCGTGAATTCGAGTTA	411	
Qy	415	ATGCGACCAATGGATCACCCAAATGTTCATCTCTTTGAAGCACTGTTTCTTCTCTACAACG	474	
Db	412	ATGCGCTTAATGGATCACCCCTAAATGTAATTTCCCTGAAGCACTGTTTCTTCTCCACAACA	471	
Qy	475	AGTAGAGATGAGCTTCTCTCAAACCTTGTGTTATGAGAGTATGTAACCTGAGACTTTATACCGG	534	
Db	472	AGCAGAGATGAACCTTTTTTCTAAAACCTTGGTATGGAATATGTTCCCGAATCAATGTACCGA	531	
Qy	535	GTTTGTGAGGCACTACTACTGTTCTAATCAGAGGATGCCAATTTTCTATGTCAAGCTTTTAC	594	
Db	532	GTTTATAAGCACTACTACTATGAACACAGAGAATGCCCTCTCATCTATGTGAAAATGTAT	591	
Qy	595	ACATATCAAAATCTTTAGAGGTTTGGCTTTACATCCATACTGTTCCCGGTGTTTGCACAGA	654	
Db	592	ACATATCAAAATCTTTAGGGATTAGCATATATCCATACCGACATGGGAGTTTGCATAGG	651	
Qy	655	GATGTGAAACCAAAAATCTCTTGGTTGATCCCTTGACCCCAATCAGGTTTAAGCTGTGTGAT	714	
Db	652	GATGTGAAGCCTCAAAATCTTTTGGTTTCATCCTCTTACTACCAAGTTTAAGCTATGTGAT	711	
Qy	715	TTTGGAAATGCCAAAAGTATTGGTCAAAGGTGAACCAAAACATATCATATATCTGCTCCCGT	774	
Db	712	TTTGGGAGTGCAAAAGTCTGGTCCAGGGTGAATCAAAACATTTTCATACATATGTTTCAAGT	771	
Qy	775	TATTATCGTGTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGATCCATAGATATA	834	
Db	772	TACTATCGGGCTCCAGAACTAATATTGTTGGCAACAGAAATACACAGCTTCTATTGATATC	831	
Qy	835	TGGTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTGGCCAGCGGTTATTTCAGAGGAA	894	
Db	832	TGGTCAGCTGGTTGTGTTCTTGTCTGAACTCTTCTAGSACAGCCATATTATTCCTGGAGAA	891	
Qy	895	AATTCAGTTGATCAGCTGTGGAGATCATTAAGGTTCTTGGTACTCCAACTCGTGAAGAA	954	
Db	892	AACCAAGTGGACCAACTTGTGGAAATTTATCAAGGTTCTTGGTACTCCAAACACGCGAGGAA	951	
Qy	955	ATTCGATGTATGAACCCGAACTACACAGATTTTATAGGTTCCACAAAATCAAGCTCACCT	1014	
Db	952	ATCCGTTGTATGAACCCAAATTTATACAGATTTTATAGTTTCCCTCAGATTAAGGCTCATCCT	1011	
Qy	1015	TGGCACAAGGTTTTTTCATAAACCGATGCCTCCAGAAGCAATPAGACCTTGTGATCTCGGCTT	1074	
Db	1012	TGGCACAAGGTTTTTCCACAAGCGAATGCCTCCTGAAGCAATTGACCTTGCATCAAGGCTT	1071	
Qy	1075	CTTCAATATTCAACCAAGCTTACGCTGCACTGCGGCTCGAAGCATGTGCTCATFCGGTTTTTC	1134	
Db	1072	CTCCAAATTTCACCTAGTCTCCGCTGCACCTGCGCTGGAAGCATGTGACATCTCTTCTTT	1131	

### RESULT 3

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US-10-437-963-98579/c
; Sequence 98579, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 98579
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96473C.1
; US-10-437-963-98579

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Query Match	44.2%	Score	713.2;	DB	19;	Length	1831;
Best Local Similarity	79.5%;	Pred.	No. 1.2e-187;				
Matches	844;	Conservative	0;	Mismatches	187;	Indels	0;
Gaps	0;						
Qy	208	GAGCGTGTACTCGTGCATATCATTTCCACTACTATAGGAGGCCAAAAACGSCGAACCAAAG	267				
Db	1591	GAGCCGTGCGGGTCAATCATCTCCACCATCGCGGGCAAGAACGGCGAGCCGAAG	1532				
Qy	268	CAGACCATTAGTTTACATGCTGACGGGTGTTTGGAAACAGGTTTCATTCGGGATGTGTTTT	327				
Db	1531	CGGACCAATTAGTTATATGCGCGGACGAGTTGTAGGAACCTGGTTCTTTCCGGATGTGTTTC	1472				
Qy	328	CAGCGCAATGCTTGGAAACTGGAGAAATCAGTAGCCATTAAAAAGCTCTTGCAGATCGA	387				
Db	1471	CAGCTAAGTGCCTTGGAGACGGGGGAAACGGTGGCCATCAAGAAGGTGTTTGCAGGACCGG	1412				
Qy	388	CGCTATAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCCAAATGTGCATCTCC	447				
Db	1411	CGTTACAAGAACCGTGAACTGACAGCTTATGCGCGCAATGGAAACACCCCAATGTCACTGC	1352				
Qy	448	TTGAAGCACTGTTTCTTCTCTACAACGAGTAGAGATGAGCTCTTCTCTCAACCTTGTTATG	507				
Db	1351	CTGAAGCACTGCTTCTTCTCAACCAACGACGGGATGAGCTGTTCTCTGAATCTTGTTATG	1592				
Qy	508	GAGTATGTACCTGAGACTTTTATACCGGGTTTTGAGGCACCTATACTAGTTCTTAATCAGAGG	567				
Db	1291	GAGTACGTCCTGAGACACTCTACCGTGTGCTCAAGCACTTACAGCAATGCTAACACGCGG	1232				
Qy	568	ATGCCAATTTTCTATGTCGAAGCTTTACATATCAAAATCTTTAGAGGTTTGGCTTACATC	627				
Db	1231	ATGCCAATGATCTATGTGAAGCTTTTACATCTATCAGCTTTTTCAGAGGGTTAGCTTATATT	1172				
Qy	628	CATACCTGTTCCCGGTGTTTTGGCCACAGAGATGTGAAACCAAAAATCTCTTGGTTGATCCC	687				





Db 201 TGCGCTGATGATAGGAGATGCCCTGCTGTAGTTGATGACATGATCAAGTCACCTGGTC 260  
QY 224 ATATCATTTTCCACTACTATAGGAGGCAAAACCGCGCAACCAAGCAGACCATTTAGTTACA 283  
Db 261 ATATTAATTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAGCAATTAGTTACA 320  
QY 284 TGCGCTGAGCGGGTGTGTGAACAGGTTCAATTCGGGATGTGTTTTCAGGCGAAATGCTTGG 343  
Db 321 TGGCGGAGCGAGTGTGTGTGTACAGGCTCGTTCGGGATCGTTTTCGAAGCAAAATGTTGG 380  
QY 344 AAAGCTGAGATCAGTAGCCATTAATAAGGCTTTGCAAGATCAGCCTATATAAACCGGTG 403  
Db 381 AGACTGGAGAAACCGTGGCGATTAAGAAGGTTTTCGAAGATAGAGATACAAGAACCGAG 440  
QY 404 AGTTGCAACTAAGCGCACCAATGGATCACCCCAATGTCATCTCTTGAAGCACTGTTTCT 463  
Db 441 AACTTCAGTTGATGCGGTGATGGATCATCCGAATGTGGTTGTTTGAAGCATTTGCTTCT 500  
QY 464 TCTCTACAACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGAGAGTATGTACCTGAGA 523  
Db 501 TTTGACTACAAGTAAGACGAGCTTTTCTTGAACCTTGGTATGAGAGTATGCCCTGAGA 560  
QY 524 CTTTATACCGGGTTTTGAGCACTATACCTAGTTCTAATCAGAGGATGCCAATTTTCTATG 583  
Db 561 GCTTGTATCGAGTTCTGAACAATATATAGTAGTGAACCAACCAAGATGCTCTTGTCTATG 620  
QY 584 TCAAGCTTTACACATATCAAACTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTG 643  
Db 621 TTAACCTTTACATGATCAGATCTTCGGGAGCTTCTTACATTCACAATGTTGCTGGAG 680  
QY 644 TTTGCCACAGAGATGTGAACCAACAAATCTCTTGTGTTGATCCCTTGACCCATCAGGTTA 703  
Db 681 TTTGTACAGAGATCTAAGACCTCAAAATCTCTGTTGATCTTACTCATCAAGTCA 740  
QY 704 AGCTGTGTGATTTTGAAGTGCAAAAGTATGTGTCAAGTGGAACCAACATATCATATA 763  
Db 741 AATCTGTGACTTTGGCAGTGGCAACAGCTCGTTAAAGGTGAAGCAACATTTCTTACA 800  
QY 764 TCTGCTCCGCTTATATCGTGTCCAGAACTCATCTTGGCGCCACAGAGTATACAGCAT 823  
Db 801 TCTGCTCACAAATCTACCGTGACCCGAGCTCATATTTGGTGCATGAGTACACAAT 860  
QY 824 CCATAGATATAGTGTCTGTGTGTGTACTGCGCAGAGCTTCTTCTTGGCAGCCGTTAT 883  
Db 861 CTATTTGATATCTGCTGTGTGTGTGTCTTCTGCTGAGCTTCTTCTTGGTCAGCATTA 920  
QY 884 TTCAGAGAGAAATTCAGTTGATCAGCTTGTGAGATCATAAAGGTTCTTGTACTCCAA 943  
Db 921 TTTCCCGAGAGAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAGTTCTTGTGTACCAA 980  
QY 944 CTGCTGAAGAAATTCGATGTATCAACCCGAACCTACACAGATTTTAGGTTCCCAACAATCA 1003  
Db 981 CTCGAGAAGAAATCCGTTGTATGAATCCCAATTACACAGATTTTCAGGTTTCCACAGATA 1040  
QY 1004 AAGCTCACCCCTTGGCAAGAGTTTTTTCATAAAGGATGCTCCAGAGCAATAGACCTTG 1063  
Db 1041 AGGCATCTCTGGCAAGATCTTCCACAAAGGATGCCCCAGAGCGATTTGATTTG 1100  
QY 1064 CATCTCGGCTTCTCAATATTCACAAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTC 1123  
Db 1101 CATCAAGGCTGCTTCAATATCTCTCAAGTCTAAGATGCAAGGCTCGAAGCTTGTGCAC 1160  
QY 1124 ATCCGTTTTTCAATGAACTCCGAGAGCCAAACCGCTCTTCCAAATGCTGCTCCATTAC 1183  
Db 1161 ATCCGTTCTTTGATGAACCTCAGAGAACCAACGCTCTGTTTACCAAATGGAAGGCTTTCC 1220  
QY 1184 CGCCATTGTTCAATTTCAAAACAAGAGTTAGGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243  
Db 1221 CGCCTCTCTTCAACTTCAAAACAAGAGTAGCTGGATCATCACTGGAATGCTCAACAAGT 1280  
QY 1244 TAATACCTGAGCATGTGAGACGACAAATGAGACAGGATT 1283  
Db 1281 TGATTCAGACCATATCAAGAGACAAATTTGGGTCTTAAGCTT 1320

RESULT 7

US-10-425-114-12807  
; Sequence 12807, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 2003-04-28  
; SEQ ID NO 12807  
; LENGTH: 1726  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701212714\_FLI  
US-10-425-114-12807

Query Match 43.8%; Score 706.2; DB 18; Length 1726;  
Best Local Similarity 76.1%; Pred. No. 18-185;  
Matches 870; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 141 CGCTTTGAAACCGCGTCCTGAATTTGGATTTCTGATAAGGAAATGCTGACAGCTGTTATTGA 200  
Db 70 CTCTCTCTCTCCCTCGCCCATGGCTGAGGATAGGAGATGTCTACCTCTGTCATCAA 129  
QY 201 GGGAAATGAGGTGTGTACTGTCATATCATTTTCCACTATATAGGAGGCAAAACCGCGGA 260  
Db 130 TGGGAATGATCCCTAACTGGTCAATCATATCTACAACTATTTGGAGGCAAAATGGGA 189  
QY 261 ACCAAGCAGACCCNTAGTTTACATGCTGAGCGGGTGTGGACAGGTTCTATTCGGGAT 320  
Db 190 ACCCAACAGACTTATTTAGCTACATGGCAACCGGGTTGTAGGAACCTGGATCATTTGGAAT 249  
QY 321 TGTTTTTCAGGCGAAATGCTTGGAACTCGGAATCAGTAGCCATTAATAAAGGCTTTTGA 380  
Db 250 CGTTTTCCAGGCAAAATGCTTGGAACTGGGAGGAGTGGCAATTTAAAGGTTTACA 309  
QY 381 AGATGACGCTATAAAACCGTGAGTTGCAACTAATGCGACCAATGGATCACCAGATGT 440  
Db 310 AGACAGAAGATACAGAATCGTGAACCTGAATTAATGCGTGTGATGGATCATCCAAATGT 369  
QY 441 CATCTCTTGAAGCACTGTTTCTTCTCTACAGGATGAGATGAGCTTCTCTCAACCT 500  
Db 370 GATCTCTTGAAGCACTGTTTCTTCTTCAACTCAAGTACAGATGAACCTTTTCTCAATTT 429  
QY 501 TGTATGAGAGTATGTACCTGAGACTTTATACCGGGTTTTGAGGCACTATATAGTTCTAA 560  
Db 430 GGTATGAGATATGTTCCAGAGTCCATGTATAGAGTCTTAAGCACTATAGCAATGCTAA 489  
QY 561 TCAGAGGATGCCAATTTTCTATGTCAAGCTTTACATATCAAACTTTTAGAGGTTTGGC 620  
Db 490 TCAAGAAATGCCAATCATCTACGTAACCTTTATATGTACCAGATTTTCAGGGGTTGGC 549  
QY 621 TTACATCATACTGTTCCCGGTGTTTGGCCACAGAGATGTGAACCAACCAAACTCTTGTGT 680  
Db 550 TTACATCCACACTGGTCCCAAAAGTTTGGCCACAGAGATTTGAAGCCCTCAAAATATCTGGT 609  
QY 681 TGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGAAGTATTTGGTCAA 740  
Db 610 GGATCTCTTACACACCAAGTGAAGCTATGTGATTTTGGAAAGTGAAGTCTTAGTCTGA 669  
QY 741 AGGTGAACCAACATATCATATATCTGCTCCCGTTATATATCGTGTCCGAGCAATCATCTTT 800



<p> <b>RESULT 9</b>            US-09-854-731-15            ; Sequence 15, Application US/09854731            ; Patent No. US20020120949A1            ; GENERAL INFORMATION:            ; APPLICANT: Allen, Steve            ; APPLICANT: Lee, Jian Ming            ; TITLE OF INVENTION: Plant Protein Kinases            ; FILE REFERENCE: BB-1171            ; CURRENT APPLICATION NUMBER: US/09/854,731            ; CURRENT FILING DATE: 2001-05-14            ; PRIOR APPLICATION NUMBER: 60/092,438            ; PRIOR FILING DATE: July 10, 1998            ; NUMBER OF SEQ ID NOS: 23            ; SOFTWARE: Microsoft Office 97            ; SEQ ID NO 15            ; LENGTH: 1673            ; TYPE: DNA            ; ORGANISM: Triticum aestivum            ; FEATURE:            ; NAME/KEY: unsure            ; LOCATION: (1349)            US-09-854-731-15         </p>									
QY	98	AGCCTCATGCTCTTGTCTGCTCCGCTGAGCTTCCAGACGCGGACGCTTTTGAACGCGTC	157						
Db	48	AGCATCGGCGCGCGCGGACCGCTGCTGCTGACGAGCAGCCGCCCGCAGTCG	107						
QY	158	CTGAATTGATTCGTATAGGAATAATGTCTGACGCTGTATTTAGGGAATGACGCTGTTA	217						
Db	108	CTGCGAGAAGAAGCAGCAGATGGCGGCGCGCTATGCGAGGGGAACGAGCCCATGA	167						
QY	218	CTGGTCATATCAATTCCTACTATAGGAGGCAAAACGCGCAACCAAGCAGACCATTA	277						
Db	168	CCGGTCACATCATCTCCACCACCATCGCGGCAAGACGCGAGCCCAAGCAGACGATTA	227						
QY	278	GTTCATGCTGACGCGGTTGTTGGAACAGGTTTCATTCGGGATGTTTTCAGGCGAAAT	337						
Db	228	GCTACATGGGAGCGGTTGTGGGACATGTTTCGTTTGGCATCGTCTTCAGGCTAAT	287						
QY	338	GCTTGAAATCGAGAAATCAGTAGCCATTTAAAGGCTTTGGAAGATCGAGCGGTATAAA	397						
Db	288	GCCTGAAACCGGGAGATGTTGGGCAATTAAGAAAGGTACTGCGAGGACAGACGGTACA	347						
QY	398	ACGCTGAGTTGCAACTAATCGCAACCAATGGATCACCCCAATGTCTCTCTGAAGCACT	457						
Db	348	ACCGTGAGCTGAGCTTATGCGTTGATGATCCATTCATGTTGTTCTCTCTCAAGCACT	407						
QY	458	GTTCCTCTCTACAACGAGTAGAGTAGCTCTCTCTCAACCTTGTATGAGGATGTATGAC	517						
Db	408	GCTTCTCTCAACCAAGTAGAGTAGGCTGTTCTCTGAACTTGTGATGATGATGTC	467						
QY	518	CTGAGACTTTATACCGGTTTTCAGGCACTATGATGATGTTCTATCTAGAGATGCCAATTT	577						
Db	468	CGGAGAGCGCTATACCGGCTGTTTAAGCACTACAGTAATGCCAACAGGGGATCCCGTTA	527						
QY	578	TCATGTCAAGCTTTACACATATCAATCTTTAGAGGTTTGGCTTACATCCATACGTTTC	637						
Db	528	TCATGTCAAGCTTTACATGTATCAGCTTTTATAGGGCTAGCTTATGTTTCATCTGTTTC	587						
QY	638	CCGGTGTTCGCCACAGAGATGTGAACCAAAAATCTCTTGGTGTATCCCTTCAGCCATC	697						
Db	588	CAGGAGTTTCCACAGGATGTGAACCAAAAATGTTTGGTGTATCCCTTAACCCATC	647						
QY	698	AGTTAAGCTGTGTATTTTGGAGTGCAAAAGTATTTGGTCAAAAGCAACATAT	757						
Db	648	AAGTCAAGATCTGTGACTTTGGAGTGCAAAAGTTCCTGGTACCTGGTGAAACCAATAG	707						

  

QY	758	CATATATCTGCTCCCGTTATTTATCTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATA	817						
Db	708	CATACATATCTCTCGTACTATCTGCTCTCTGAGCTCATATTTGGTGAACCTGATATA	767						
QY	818	CAGCATCCATAGATATATGCTGCTGCTGTTGTACTGGCAGAGCTTCTTCTTGGCCAGC	877						
Db	768	CAACTTCAATAGACATATGCTCAGCTGGATGTTCTTTCAGAGCTACTTCTTGGTCCAGC	827						
QY	878	CGTTATTTCCAGAGAGAAATTCAGTTGATCATGCTGTTGGAGATCATAAAGGTTCTTGTA	937						
Db	828	CTCTGTTTCCAGAGAGAGACTGCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGTGA	887						
QY	938	CTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGGTTCCAC	997						
Db	888	CTCCAACTCGTGAAGAAATTCGTCATGAACCCCACTATACCGAGTTTCAGGTTTCTCTC	947						
QY	998	AAATCAAGCTCACCCCTTGGCAAGGTTTTCATAAACCAGATGCTCCAGAAAGCAATAG	1057						
Db	948	AGATTAAAGGCTCATCTTGGCAAGATTTTCCCAAGAGAAATGCCCGCTGAAGCTATAG	1007						
QY	1058	ACCTTGATCTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGCGCTCGAGCAT	1117						
Db	1008	ATCTTGCTCCCGCTTCTCCAGATTTCCAAATCTACGTTGCACTGCTCTTGTATGAT	1067						
QY	1118	GTGCTCATCCGTTTTCATGAACCTCCAGAGAGCAAAACCCCGCTCTTCCAAATGGTCTC	1177						
Db	1068	GTGCAATCTCTTCTTGTATGAGCTACGTGAGCGCAATGCAAGCTTGCAGATGGCGCC	1127						
QY	1178	CATTACCGCCATGTTTCAATTTCAAACAAGATTTAGGTGGAGCTTCAATGGAGCTAATCA	1237						
Db	1128	CATTCCCTCTCTGTTTCAATTTCAAACCTGAACTAGCAAGCGCTCTCCAGAGCTCATCA	1187						
QY	1238	ACAGGCTATATCTGAGCATGTGAGACGCAATGAGCAC	1277						
Db	1188	ACAGGCTTGTTCGGAACATGTTTCGACGCAAAATGGCCC	1227						

  

<p> <b>RESULT 10</b>            US-10-424-599-67987            ; Sequence 67987, Application US/10424599            ; Publication No. US20040031072A1            ; GENERAL INFORMATION:            ; APPLICANT: La Rosa Thomas J            ; APPLICANT: Kovalic David K            ; APPLICANT: Zhou Yihua            ; APPLICANT: Cao Yongwei            ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With            ; FILE REFERENCE: 38-21(53223)B            ; CURRENT APPLICATION NUMBER: US/10/424,599            ; CURRENT FILING DATE: 2003-04-28            ; NUMBER OF SEQ ID NOS: 285684            ; SEQ ID NO 67987            ; LENGTH: 1881            ; TYPE: DNA            ; ORGANISM: Glycine max            ; FEATURE:            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32405C.1            US-10-424-599-67987         </p>									
<p>           Query Match 43.4%; Score 699.8; DB 18; Length 1881;            Best Local Similarity 75.8%; Pred. No. 6.5e-184;            Matches 866; Conservative 0; Mismatches 277; Indels 0; Gaps 0;         </p>									
QY	141	CGTTTGAACCGCGCTCTGAATTTGGAATTTCTGATAAGGAAATGCTGCGAGCTTTATTGA	200						
Db	112	CTCTCTCTCTCTCCCTCCCGCATGGCTGAGGATAAGGAGATGCTACCTCTCTCATCA	171						
QY	201	GGGAATGAGCTGTTTACTGTCATATCTTCCACTACTATAGGAGGCAAAACGCGCA	260						
Db	172	TGGGAATGATTCCTCAACTGGACACATATCTCACTATTTGGAGGCAAAATGGGA	231						
QY	261	ACCAAGCAGACCATTTAGTTTACATGCTGAGCGGGTGTGGAACAGGTTTCATTCGGAT	320						

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Db 232 ACCCAACAGACTATTAGTTTACATGCGAAGCGGGTTGTAGGAACCTGGATCATTTGGAAAT 291
Qy 321 TGTCTTTTCAGGCGAAATGCTTGGAAACCTGAGGAATCAGTAGGCCATTAATAAGAGCTTGTGCA 380
Db 292 TGTCTTTTCAGGCGAAATGCTTGGAAACCTGAGGAGCGAGTGGCAATTAATAAGAGCTTGTGCA 351
Qy 381 AGATCGACCTATAAAACCGGTGAGTTGCAACTAATGCGAACCAATGAGTACCCCAAAATGT 440
Db 352 AGACAGAAGATACAAGAATCGTGAACACTACAGTTAATGCGTGTGATGGATCATCCAAATGT 411
Qy 441 CATCTCTTGAAGCACTGTTCTCTCTCAACAGAGTAGAGATGAGCTCTTCTCTCAACT 500
Db 412 GATCTCTTGAAGCACTGTTCTCTCTCAACAGAGTAGAGATGAGCTCTTCTCTCAACT 471
Qy 501 TGTATTGAGGATATGACCTGAGACTTTATACCGGGTTTTGAGGCACTATACCTAGTTCTTAA 560
Db 472 GGTGATGAGGATATGTTCCAGAGTCCATGTATAGAGTCTTTAAGCACTACAGCAATGCTAA 531
Qy 561 TCAGAGGATGCCAATTTCTATGTCAAGCTTTACACATATCAAAATCTTTAGAGGTTTGGC 620
Db 532 TCAAGAAATGCCATCATCTACGTTTAACTTATATATGATGACCAAGATTTTCAGGGGGTTGGC 591
Qy 621 TTACATCCATACGTCTCCGGGTGTTTGCACAGAGATGTGAACCAACCAAAATCTCTTGGT 680
Db 592 TTATATCCACACTGTTCCCAAGTTTGGCACAGAGATTTGAAGCCTCAAAATATATACTGGT 651
Qy 681 TGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGAAGTGCAGAAAGTATTCGTCAA 740
Db 652 GGATCCTCTTACACCAAGTGAAGCTATGTGACTTGTGAAGTGCAGAAAGTATTCGTCAA 711
Qy 741 AGGTGAACCAACATATCATATATCTGCTCCGGTTATATCTGCTTCAGAACTCATCTT 800
Db 712 AGGTGAAGCTAATATATCATATATGTTTCAAGTCTTATCGAGTCTTATCGAGCACCAGAACTCATAT 771
Qy 801 TGGCGCCACAGAGTATACAGATCCATAGATATATGCTCTGCTGCTGTTGTGACTGGCAGA 860
Db 772 TGGCGCCACAGAGTATACAGATTCATATGATTTGGTCAAGTGTGCTGCTGCTTGTGCTGGA 831
Qy 861 GCTTCTCTTGGCGCAGCGGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGAT 920
Db 832 ACTTCTTTTGGCGCAGCCATTTATCCCTGGCGAAATTCGAGTAGACAGCTGTGTACATAT 891
Qy 921 CATAAAGGTTCTGTGATCTTCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACAC 980
Db 892 TATAAAGGTTCTGTGACCGCCACTCGAGAGGAAGTACGCTGTATGAATCCCAATTAACA 951
Qy 981 AGATTTTGTGCTCCCAAAATCAAAAGCTCACCTTGGCACAGGTTTTTTCATAAACGGAT 1040
Db 952 TGACTTTTGTGCTCCAGATAAAAGCACCCATGGGCACAGATATTTCCACAAAGAT 1011
Qy 1041 GCCTCCAGAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTG 1100
Db 1012 GCCTCCGAGAGCTATGTGATCTCGATCCGGCTGTGTGATCTCCCAAGTCTCCGGTG 1071
Qy 1101 CACTGCGCTCGAAGCATGTGCTCATCCGTTTTTCAATGAACCTCGAGAGCCAAACGCCCG 1160
Db 1072 CACTGCACTTGAAGCATGTGCACATCTCTTTTGTGATGAACCTTGTGTAACCAACGCTCG 1131
Qy 1161 TCTTCCAAATGGTGTGCTCATATCCGCCATTTGTTCAATTTCAAAAGAGTTAGTGGAGC 1220
Db 1132 CCTGCAATGGTGTGCTCATATCCGCCATTTTCCCTCTTATTTAACTTCAAAAGAGTTATCTGGAGC 1191
Qy 1221 TTCAATGAGCTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCACAGG 1280
Db 1192 ATCTCCGAGCTTGTTAATAGTTGATACCTGACCATGTGAAGCGGCAATGGGGCTACA 1251
Qy 1281 ATT 1283
Db 1252 ATT 1254
```

RESULT 11

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US-10-424-599-67989
; Sequence 67989, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67989
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32407C.1
US-10-424-599-67989
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Query Match 43.3%; Score 699.2; DB 18; Length 1744;
Best Local Similarity 77.5%; Pred. No. 9.2e-184;
Matches 859; Conservative 0; Mismatches 248; Indels 1; Gaps 1;

Qy 164 TGGATTTCTGATAAGGAAATGTCGAGCTGTTATTGAGGGAATGACGCTGTACTGTGTC 223
Db 123 TGGCTGAGGATAAGGAGATGCTTCTCTGTGTCACCAATGGCGATGATCTCTCACTGGCC 182
Qy 224 ATATCATTTTCCACTACTATAGGAGCAAAACCGGGAACCCAAAGCAGACCATTAGTTACA 283
Db 183 ACATCATATCTACAACATATTGGAGGCAAAATGGGGAACCCAAACAGACTATTAGTTACA 242
Qy 284 TGGCTGAGCGGTTGTTGGACAGGTTTCATTCGGGATGTTTTCAGCGGAATGCTTGG 343
Db 243 TGGCTGAACGGGTTGTAGGAATCGATCATTTTGGAAATGTTTTCAGGCAAAATGTTGG 302
Qy 344 AAACCTGGAAGATCAAGTACCCATTAAGAGCTCTTCAAGATCGACGCTATATAAACCCGTG 403
Db 303 AAACCTGGGAGCAGTGGCCATTAAGAGTTTACAGACAGAGATACAAGATCGTG 362
Qy 404 AGTTGCAACTAATGCGACCAATGGAATACCCAAATGTCTCTTGAAGCACTGTTTCT 463
Db 363 AACTACAGTTAATGCTGTTTGGATCATCCAAATGTCTCTCTGAAGCACTGTTTCT 422
Qy 464 TCTCTACAAACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGAGATGTACCTGAGA 523
Db 423 TTTCAACTACAAAGTACAGATGAGCTTTTCTTAATTTGGTATGGAATATGTTCCAGAGT 482
Qy 524 CTTTATACCGGGTTTGAAGGCACTATACCTAGTTCTTAATCAGAGGATGCAATTTTCTATG 583
Db 483 CCATGTATAGAGTCATTAAGCACTATATACTAATGCTTAATCAAGATGCCAATCATCTATG 542
Qy 584 TCAAGCTTTACATATCAAAATCTTTAGAGTTTGGCTTACATCATCATCTGTTCCGGTG 643
Db 543 TAAACCTTTACATGTACAGATTTTCAGGGATTTGGCTTATATCCACACTGTTCCCAAG 602
Qy 644 TTTGCCACAGAGATGTGNAACCAAAATCTCTTGGTTGATCCCTTGAACCCATCAGTTA 703
Db 603 TTTGCCACAGAGATTTGAAGCCTCAAAATATATCTGTTGGATCTCTTACACACCAAGTGA 662
Qy 704 AGCTGTGTGATTTTGAAGTGCAGAAAGTATTGGTCAAGGTTGAACCAACATATCATATA 763
Db 663 AGCTATGTGATTTTGAAGTGCAGAAAGTCTTAGTAAAGGTTGAGCTAATATATCATACA 722
Qy 764 TCTGCTCCCGTTATATCGTCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCAT 823
Db 723 TATGTTACAGATTTCTATCGCGCTCCAGAACTTATATTATTTGGCGCCACAGAGTATACA 782
Qy 824 CCATAGATATATGTTCTGCTGGTTGTGTACTGGCAGAGCTCTTCTTGGCGCCAGCGTTAT 883
Db 783 CAATTGATATTGTTGCTGCTGCTGTGCTTCTTGTGAACTTCTTTTGGGCCAGCCATTAT 842
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;; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS  
;; TITLE OF INVENTION: OF USE IN PLANTS  
;; FILE REFERENCE: 16313-0178  
;; CURRENT APPLICATION NUMBER: US/10/292,408  
;; PRIOR FILING DATE: 2002-11-12  
;; PRIOR APPLICATION NUMBER: 60/346,096  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 51  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 1499  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
US-10-292-408-21

Query Match 43.0%; Score 693.4; DB 16; Length 1499;  
Best Local Similarity 76.2%; Pred. No. 3.5e-182;  
Matches 853; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 152 GCCGCTCGAATGGATTCTGATAAGGAATGTCTGACGCTGTTATTTAGGGAATGACG 211  
DB 153 GCGGCTCCGACCGCGCACGAAAGGAATGTCTGCTCGCAGATGGTAATGATG 212

QY 212 CTGTTACTGCTCATATCTTCCACTATATAGGAGGCAAAACGCGCAACCAAGCAGA 271  
DB 213 CACTCACTGGTCACTAATCTCAACCAATTTGCGAGGCAAAATGCGCAACCTAAACAA 272

QY 272 CCATTAGTTTACATGGCTGAGCGGGTGTGGAAACAGGTTTCAATCGGGATGTTTTCAGG 331  
DB 273 CCATCAGTTTACATGGCGCAACGTTGTTGGCACTGGATCAATTTGCCATGTTTCCAGG 332

QY 332 CGAATGCTTGAACATGGAGAACTAGTAGCCATTAATAAGTCTTGAAGATCGACGCT 391  
DB 333 CGAAGTCTTGGAGACTTGGCGAGGAGTGGCTATATAAGAAAGTCTTTCAGGACAGCGCAT 392

QY 392 ATAAAAACGTCAGTTGCAACTAATGCGACCAATGATCACCACCAATGTCTCTCTTGA 451  
DB 393 ACAAAATCGTGAACGTTGTAATGCGCGTATGATCACCACCAATATAATTTCTTGA 452

QY 452 AGCACTGTTTCTCTACACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGGAGT 511  
DB 453 GTAACATTTCTCTACACAGTAGAGATGAACTTTTCTGAACTTGGTATGGAT 512

QY 512 ATGTACTGAGACTTTATACCGGTTTGGAGCACTATATAGTTCTTAATCAGAGATGC 571  
DB 513 ATGTCCCTGAGACGATCTTCCGTTTATAAAGCACTACAGTAGCATGAAACAGAGAAATGC 572

QY 572 CAATTTCTATGCTCAAGCTTTACATATCAATCTTTAGAGTTTGGCTTACATCCATA 631  
DB 573 CCTAATCTATGTGAATTTATATACATATCAATCTTTAGGGGACTTGGCGTATATCCATA 632

QY 632 CTGTTCCGCGTGTGGCCACAGAGATGTGAACCAACCAAAATCTTTGGTTGATCCCTTGA 691  
DB 633 CTGTACCAAGGAATCTGCCATAGGAATTTGAAGCTTCAAAATCTTTGGTTGATCACTCA 692

QY 692 CCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGCAAAAGTATTTGGTCAAGGTGAACAA 751  
DB 693 CACACCAAGTCAAGCTGTGTGATTTTGGAGTGTCAAAAGTCTCTGTGGAGGGTGAATCAA 752

QY 752 ACATATCATATATCTGCTCCGTTTATATCGTGTCCAGAACTCATCTTTGGCGCCACAG 811  
DB 753 ACATTTTACATATATGTTTCAACGTTACTATCGTGGCCCAAGAGCTAATATTTGGTGGCGGAG 812

QY 812 AGTATACAGCATCCATAGATATATGCTGCTGCTGTTGTGTACTGCGCAGAGCTTCTTCTTG 871  
DB 813 ATACACAACTTCTGTGTATTTTGGTCCGCTGTTGTGCTCTCGGAACTTCTTCTAG 872

QY 872 GCCAGCGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCAATAAGGTTTC 931  
DB 873 GCCAGCTTTGTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAAATTAATCAAGATTC 932

QY 932 TTGGTACTCAACTCGTGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTAGT 991

## RESULT 14

US-10-424-599-26109  
; Sequence 26109, Application US/10424599  
; Publication No. US20040031072A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 26109  
; LENGTH: 1553  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAR\_MRT3847\_123578C.1  
US-10-424-599-26109

Query Match 43.0%; Score 693.4; DB 18; Length 1553;  
Best Local Similarity 76.2%; Pred. No. 3.6e-182;  
Matches 853; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 152 GCCGCTCGAATGGATTCTGATAAGGAATGTCTGACGCTGTTATTGAGGGAATGACG 211  
DB 214 GCGCTCCGACCGCGCACCGAAAGGAATGTGAGCTCTGTCGAGATGGTATGATG 273

QY 212 CTGTTACTGCTCATATCAATTTCCACTACTATAGGAGGCAAAACGCGCAACCAAGCAGA 271  
DB 274 CACTCACTGGTCACATATCTCAACCAATTTGCGAGCAAAATGCGCAACCTAAACAAA 333

QY 272 CCATTAGTTTACATGCTGAGCGGGTGTGGAAAGTTCATTTCGGGATGTTTTCAGG 331  
DB 334 CCATCAGTTTACATGCGCGAATGTTGTTGGCACTGGATCAATTTGGCATTTGTTTCCAGG 393

QY 332 CGAATGCTTGGAACTCGAGAACTAGTAGCCATTTAAAGGTCTTTGAAGATCGACGCT 391  
DB 394 CGAAGTCTTGGAGACTTGGCGAGCGAGTGGCTATATAAGAAAGTCTTTCAGGACAGCGAT 453

QY 392 ATAAAAACCGTGAGTTGCAACTAATGCGAACCAATGGATCACCAGTGTCTCTCTTGA 451  
DB 454 ACAAAATCGTGAACCTGAGTTAATGCGCGTATGAGTCAACCAATATATTTCTTGA 513

QY 452 AGCACTGTTTCTCTTCAACAGGATAGAGATGAGCTCTTCTCAACCTTGTATGGAGT 511  
DB 514 GTAACATTTCTTCTTCAACAGATAGAGATGAACATTTTCTGAACTTGGTATGGAT 573

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QY 512 ATGTACCTGAGACTTTATACCGGTTTTCAGGCACTATATAGTCTTCTAATCAGAGATGC 571
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 574 ATGTCCCTGAGAGCATCTCCGGTGTATTAAGCACTACAGTAGCATGAACAGAGATGC 633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 572 CAATTTCTATGTCAAGCTTTACACATATCAAACTTTTAGAGGTTTGGCTTACATCCATA 631
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 634 CCTAATCTATGTGAATATATACATATCAAACTTTTAGGGGACTGGCGTATATCCATA 693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 632 CTGTTCCCGGTGTTTGGCCACAGAGATGTGAACCAAAATCTCTTGGTTGATCCCTTGA 691
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 694 CTGTACCAAGAACTCTGCCATAGGATTTGAAGCTCAAAATCTTTTGGTTGATCCGACTCA 753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 692 CCATCAGGTAGCTGTGATTTTGGAGTGCRAAGTATTTGGTCAAGGTGAACCAA 751
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 754 CACCAAGTCAAGCTCTGTGATTTTGGAGTCAAAAGTCTCTGGTGGAGGTGAATCAA 813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 752 ACATATCATATATCTGCTCCCGTTATATATCGTGTCTCCAGAACTCATCTTTGGCGCCACAG 811
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 814 ACATTTACATATATGTTCAAGCTACTATCGTGCCCGCAGAGCTAATATTTGGTGGCGAG 873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 812 AGTATACAGATCCATAGATATATGCTGTGCTGTGTTGTGTACTGGCAGAGCTTCTTCTTG 871
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 874 AATACAAACTCTGTGTGATTTTGGTCCGCTGTGTTGTCTTGGGAACTTCTTCTAG 933
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 872 GCCAGCGGTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 931
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 934 GCCAGCGTTTGTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 993
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 932 TTGGTACTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTGGT 991
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 994 TTGGCACTCTACTCGAGAAGAAATTCGATGATGAATCCTAATATACAGATTTTCAGAT 1053
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 992 TCCCAAAATCAAAGCTCAACCTTGGCAACAAGTTTTTCATAAACGGATGCTTCCGAGAG 1051
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1054 TCCCAATATCAAAGCTCACTCTTGGCAAAAGTTTTTCACAAGCGAAATGCTTCTGAA 1113
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1052 CAATAGACCTTGCATCTCGCTTCTTCAATATTCACCAAGTCTACGCTGCATCGCGCTG 1111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1114 CAATGACCTTGCATCAAGCTTCTCAATATTTCCCAAACTTCGTTACAGTGCAGTGG 1173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1112 AAGCATGTGCTCATCCGTTTTCATGAATCCGAGAGCAAAACGCCGCTTTCCTCAATG 1171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1174 AAGCAATGGACATCTCTTTCGACGAGCTTCGCGAGCCCAATGCTTACCTAATG 1233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1172 GTGCTCATTAACCGCATTTTCAATTTTCAAAAGATTTAGTGGAGCTTCAATGGAGC 1231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1234 GTGCTCACTGCTCCACTTTTCAACTTTAAACAGGAAITTAGATGGAGCGCCCTGAA 1293
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1232 TAATCAACAGGCTAATACCTGAGCATGTGAGAGCAAAA 1270
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 15

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US-10-425-115-22950/c
; Sequence 22950, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22950
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Zea mays

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FEATURE:

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; OTHER INFORMATION: Clone ID: MRT4577_120933C.1
US-10-425-115-22950

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Query Match 42.4%; Score 684; DB 20; Length 1779;
Best Local Similarity 76.9%; Pred. No. 1.6e-179;
Matches 834; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

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Job time : 1743.22 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: June 23, 2005, 10:16:02 ; Search time 8015.32 Seconds  
(without alignments)  
7664.793 Million cell updates/sec

Title: X99696  
Perfect score: 1614  
Sequence: 1 AGCAAGAGAGAGAGAAAA.....CCAAAAA.....AAAAA 1614

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_hc.\*
- 4: gb\_est3.\*
- 5: gb\_est4.\*
- 6: gb\_est5.\*
- 7: gb\_est6.\*
- 8: gb\_gss1.\*
- 9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1293.2	80.1	1461	3	CNS0AB1V	BX817800 Arabidops
2	1284.6	79.6	1409	3	CNS0AB1V	BX815323 Arabidops
3	713.2	44.2	1197	9	CL957492	CL957492 OsIFCC000
4	676	41.9	1745	3	AY106255	AY106255 Zea mays
5	665	41.2	1666	3	AY104068	AY104068 Zea mays
6	635.4	39.4	924	7	CK266410	CK266410 EST172488
7	603.4	37.4	620	1	AV827407	AV827407 AV827407
8	584.4	36.2	1967	3	AY103545	AY103545 Zea mays
9	581.8	36.0	932	7	CV290871	CV290871 aof01-15m
10	576.6	35.7	2295	9	CL964803	CL964803 OsIFCC011
11	575	35.6	910	7	CK290108	CK290108 EST1752830
12	574	35.6	1638	3	CNS09XSF	BX81446 Arabidops
13	572.2	35.5	591	1	AV831097	AV831097 AV831097
14	572	35.4	829	6	CB971865	CB971865 CAB10006
15	551.4	34.2	1752	3	AY108486	AY108486 Zea mays
16	551.2	34.2	963	7	CK286429	CK286429 EST749151
17	549.2	34.0	952	7	CK289285	CK289285 EST752007
18	547.4	33.9	1275	9	CL963186	CL963186 OsIFCC008
19	547	33.9	944	7	CK290066	CK290066 EST752788
20	540.6	33.2	887	6	CD574542	CD574542 UCRPT01.0
21	536	33.2	1604	3	CNS0A4PT	BX823861 Arabidops
22	533.4	33.0	876	7	CF208184	CF208184 CAB20003
23	532	33.0	853	7	CK286080	CK286080 EST748802
24	529	32.8	2036	3	CNS0A425	BX826501 Arabidops

25	528.8	32.8	936	7	CK296951	CK296951 EST759665
26	526	32.5	1870	3	CNS0ADOL	BX813745 Arabidops
27	524.2	32.5	821	6	CB894470	CB894470 EST647262
28	521.6	32.3	910	7	CK273024	CK273024 EST719102
29	515.2	31.9	926	7	CK269187	CK269187 EST715265
30	513	31.8	727	6	CD815282	CD815282 BN15.025M
31	511.8	31.7	935	7	CK276925	CK276925 EST723003
32	508	31.5	1667	3	CNS0A5F6	BX823376 Arabidops
33	505	31.3	730	7	CV051935	CV051935 EST11383
34	503.4	31.2	757	7	CK319050	CK319050 X9P06D01
35	502.2	31.1	934	7	CK266742	CK266742 EST712820
36	501	31.0	790	7	CO107864	CO107864 GR_Eb003
37	500.4	31.0	919	7	CK273361	CK273361 EST719439
38	494.8	30.7	700	6	CD835684	CD835684 BN45.046F
39	494.6	30.6	789	7	CO120041	CO120041 GR_Eb023
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41	491.2	30.4	841	7	CF515381	CF515381 CAP0001.I
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43	488	30.2	704	7	CNS08425	CNS08425 O30121ABL
44	486.4	30.1	1810	3	CNS0ADRT	BX814445 Arabidops
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## ALIGNMENTS

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LOCUS CNS0AB1V 1461 bp mRNA linear HTC 06-FEB-2004  
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLSLSL42ZC04 of Silique of strain col-0 of Arabidopsis thaliana (thale cress).  
ACCESSION BX817800  
VERSION BX817800.1 GI:42471112  
KEYWORDS HTC; GSLT cDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1461)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) Web : www.genoscope.cns.fr)  
COMMENT The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full length  
http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.  
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DB	61	ATGCTCTTCTCCGCGCTGACGCTTACAGCGGCGAGCTTTGAAACGCCGCTCTGAAT	120		
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QY	224	ATATCATTTCCACTACTATAGAGGCAAAACCGGCGAACCAGACAGACCATAGTTACA	283		
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QY	284	TGGCTGAGCGGCTTCTGGAACAGGTTCAATTCGGGATGTTTTTCAGGCGAAATCTTGG	343		
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LOCUS					
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		OSIFCC00689 Oryza sativa Express Library Oryza sativa (indica			
		cultivar-group) genomic, genomic survey sequence.			
ACCESSION		CL957492			
VERSION		CL957492.1 GI:52369867			
KEYWORDS		GSS.			
SOURCE		Oryza sativa (indica cultivar-group)			
ORGANISM		Oryza sativa (indica cultivar-group)			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
		Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE		1 (bases 1 to 1197)			
AUTHORS		Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,			
		Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,			
		Wong, G. K. S., Deng, X. W. and Wang, J.			
TITLE		An analysis of transcriptional regulation of the rice genome and			
		its comparison to Arabidopsis			
JOURNAL		Unpublished (2004)			
COMMENT		Contact: Chen Chen			
		Department of Bioinformatic			
		Beijing Institute of Genomics			
		Chinese Academy of Sciences, Beijing 101300, China			
		Tel: 86-10-80481559			
		Fax: 86-10-80488676			
		Email: chenchen@genomics.org.cn			
		Rice genomic sequence.			
		Class: exon-trapped.			
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Matches 844; Conservative		0; Mismatches 218; Indels 0; Gaps 0;			
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DB	103	GACGCGTGACGGGTCAATCATCTCCACCACCATCGCGCGCAAGAACGGGAGCCGAAG	162		

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 QY 463 ATGCCAATGATCTATGAGCTTTTACATCTATCAGCTTTTTCAGAGGTTAGCTTATAT 522  
 DB |||||  
 QY 628 CATACTGTTCCCGGTGTTGGCCACAGAGATGTGAACCAAAATCTCTTGGTTGATCCC 687  
 DB |||||  
 QY 523 CATACTGTTCCAGAGTCTGCCACAGGATGTGAACCAAAATGTTTGGTTGATCT 582  
 DB |||||  
 QY 688 TTGACCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGCAAAAGTATTTGGTCAAAAGTGA 747  
 DB |||||  
 QY 583 CTCACCTCATCAAGTCAAGCTATGTGACTTTTGGAAAGTGCAAAAGTCTGTTCTCGTGA 642  
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 QY 748 CGAAACATATCATATATCTGCTCCGTTATATCTGCTCCAGAACTCATCTTTGGCGCC 807  
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 QY 643 CGAAACATATCATATATTTGCTCTGCTATATATCTGCTCTGAGCTCATATTTGGTGCA 702  
 DB |||||  
 QY 808 ACAGAGTATACAGCATCCATAGATATATGCTGCTGTTGTTGCTAGTGGCAGAGCTTCTT 867  
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 QY 703 ACCGAGTATACACTTCAATTGACATATGTCAGCTGGATGGTCTTTCGAGAGTTACTT 762  
 DB |||||  
 QY 868 CTTGGCCAGCGGTTATTTCCAGAGAGAAATTTCAAGTTGATCAGCTTGTGGAGATCATAAAG 927  
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 QY 763 CTTGGTCAGCCACTGTTCTCGGAGAGAGTGTGTTGACAGCTAGTAGAGATAATCAAG 822  
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 QY 928 GTTCTTGGTACTCCAACCTGTTGAAGTTCGATGATGATGATGATGATGATGATGATGATG 987  
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 QY 823 GTTCTTGGTACTCCAACCGGTGAGGAAATACGATGATGATGATGATGATGATGATGATG 882  
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 QY 1108 CTGAAGCATGTGCTCATCGTTTTTCAATGAAGTCTGGAGAGCAAAAGCGGCTCTTCCA 1167  
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 QY 1003 CTTGAGCGCATGTGCATTTCTTCTTGTATGAGCTAGCAGAGGCCAATGACAGCGCTGCCA 1062  
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 DB |||||  
 QY 1228 GAGCTAATCAACAGGCTTAATACCTGAGCATGTGAGACGACAA 1269  
 DB |||||  
 QY 1123 GAACATCATCAGAGGCTCATACCGGATCATATCAGACGGCAA 1164  
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RESULT 4  
 AY106255  
 LOCUS

AY106255 1745 bp mRNA linear HTC 16-OCT-2002

DEFINITION Zea mays PCO077512 mRNA sequence.  
 ACCESSION AY106255  
 VERSION AY106255.1 GI:21209333  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1745)  
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
 Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
 Unpublished (2002)  
 REFERENCE 2 (bases 1 to 1745)  
 Coe,E.H.  
 Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; tigr, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
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 /clone\_lib="Maize Mapping Project/DuPont Consensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

## ORIGIN

Query Match 41.9%; Score 676; DB 3; Length 1745;  
 Best Local Similarity 76.5%; Pred. No. 1e-164;  
 Matches 829; Conservative 0; Mismatches 255; Indels 0; Gaps 0;  
 QY 185 CTGCAGCTTTAFTGAGGAAATGACGTGTCTGTTTACATATCATATTCCTCACTACTATAG 244  
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 QY 208 CTGGTTCTATGATTGAAGGAGTGATCCGGTCAAGGCCATATAATCTCGCAACCAATTG 267  
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 QY 245 GAGGCAAAACCGCGAACCAAGACGACCATTTAGTTACATGCTGAGCGGTTGTTGGAA 304  
 DB |||||  
 QY 268 GAGGGAAGAATGGAGAGCCTTAAAGGACTATCAGCTACATGGCAGAGAGTTGTGGAA 327  
 DB |||||  
 QY 305 CAGGTTCACTTCGGGATTGTTTTCAGGCGAAATGCTTGGAACTGGAGAAATCAGTAGCCA 364  
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 QY 328 CTGGATCATTTGGAATCGTCTTCCAGGCAAAATGCTCGAGACTGGTGAGACTGTTGCCA 387  
 DB |||||  
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 QY 425 TGGATCACCACCAATGTCTCTCTTGAAGCACTGTTCTCTCTCAACAGGATGAGAGTGC 484  
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 QY 485 AGCTCTTCTCAACCTTGTATTGAGGATGATGATCTACCTGAGACTTTTATACCGGTTTTCAGGC 544  
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 QY 508 AACTTTTCTTAACTTAGTGATGGAGTTGTTCCCGAGTCATTATATCGGGTGTGAAC 567  
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 QY 545 ACTATACTAGTTCTTAATCAGAGATGCCAATTTTCTATGTCAAGCTTTTACACATATCAA 604  
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Db 568 ATTACAGCAATATGAACAGAGGATGCCACTCATTTATGTCAAATATATATACCTACCAGA 627
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QY CACAAATCTCTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTGGAGTG 724
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QY TGAACCCGAATACACAGATTTTAGGTTCCCAAAATCAAAAGTCACTCCCTTGGCAAGG 1024
Db TGAATCCAAATACACAGGTTTAGATTTTCCCTCAGATCAAAAGTCACTCCCTTGGCAAG 1047
QY TTTTTCATAAACGGATGCTCCAGAGCAATAGACCTTGCATCTGGCTTCTTCAATAT 1084
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QY GAGAGCAAAACCCCGCTTCTCCAAATGGTCCGTCATACCGGCAATTTGTCATTTCAAC 1204
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QY 1265 GACA 1268
Db 1288 GGCA 1291

RESULT 5
LOCUS AY104068 1666 bp mRNA linear HTC 16-OCT-2002
DEFINITION Zea mays P0083097 mRNA sequence.
ACCESSION AY104068
VERSION AY104068.1 GI:21207146
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 1666)
AUTHORS Hailey C.F., Dolan M., Miao G.H., Vogel J.M., Whiteitt, M.S.,
Arthur L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1666)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of

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Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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            /db_xref="taxon:4577"
            /clone_lib="Maize Mapping Project/DuPont Consensus
            Library"
            /note="this sequence is part of a project of EST
            assemblies resulting from the application of public
            configs to seed DuPont parts; this resource was
            assembled by DuPont as part of a collaboration for the
            overgo addressing of BACs in conjunction with the Maize
            Mapping Project"
ORIGIN
    Query Match 41.2%; Score 665; DB 3; Length 1666;
    Best Local Similarity 75.4%; Pred. No. 7.3e-162;
    Matches 827; Conservative 0; Mismatches 270; Indels 0; Gaps 0;
QY 199 GAGGAAATGACGCTGTACTGTGCATATCATTTCCACTACTATAGGAGGCAAAACGCG 258
Db 260 GNAGGGGAGAGCGTGTGACGGTGCATCATCTCCACCACCATCGCGGGAGAACGCG 319
QY 259 GAACCAAGCAGACCATTTAGTTACATGCTGAGCGGTTGTTGGAACAGGTTTCATTCGG 318
Db 320 GAGCCCAAGCGACCATCAGTTACATGTCAGAACCTGCTGCTGGTACGGGCTCATTTGG 379
QY 319 ATTGTTTTTTCAGCGAAATGCTTGAAGACTGAGAAATCAGTAGCCATTAAGAGGCTTG 378
Db 380 ATCGCTTTCCAGGCTAAGTGTGTTGGAGACTGGAGAGACCTTCGCCATTAAGAGGCTG 439
QY 379 CAAGATCGACGCTATAAAACCGTCAGTTGCAACTAATGCGACCAATGATGATCACCAC 438
Db 440 CAGGATCGGCTTACAGAACCGGAGCTGCAACTTATGCTGCTGATGAGCAGCCCAAC 499
QY 439 GTCATCTCTTGAACACTGTTTCTTCTCAACAGAGTAGAGATGAGCTTCTTCTCAAC 498
Db 500 GTCATCTGCTGAACACTGTTTCTTCTCAACAGCAGCAGGAGGAGTTGTTCTTAAC 559
QY 499 CTGTATGAGAGTATGTATACCTGAGACTTTTATACCGGGTTTGGAGGCACTATAGTCT 558
Db 560 CTTGTATGGAATTTGTCCCGAGACCCCTGTACCGTGTCTGAAGCACTACAGCAACGCG 619
QY 559 AATCAGAGGATGCCAATTTTCTATGTCAGCTTTTACACATATCAATCTTTAGAGGTTG 618
Db 620 AACAGAGGATGCCCTTATCTACGCTCAAGCTCTACATGTATCAGCTTTTCAGAGCCTA 679
QY 619 GCTTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTGAACCCACAAATCTCTTG 678
Db 680 GCCTATATTCATATGTACAGGAGTCTGCCATAGGATGTAAAGCCACAAACGTTTG 739
QY 679 GTTGATCCCTTGACCCATCAGTTAAGCTGTGTGATTTTGGAGTGCAAAAGTATTTGGTC 738
Db 740 GTTGATCTCTCACCCACGAGTCAAGCTCTGTGACTTTGGTAGGCCAAAAGTCTCTGAT 799
QY 739 AAAGTGAAACCAACATATATATCTGCTCCCGTATATCTGCTGCTCCAGCAATCATC 798
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QY 799 TTTGGCGCCACAGAGTATACAGCATCCATAGATATATGCTCTGCTGTTGTGTACTGGCA 858
Db 860 TTTGGAGCGAGGAGTATACAACTTCATATAGACATATGTCAGCTGGCTGTGTTCTAGT 919
QY 859 GAGCTTCTTCTTGGCCAGCCGTTATTTCCAGAGAAATTCAGTTGATCAGCTTGTGGAG 918

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Db 920 GAGTGTCTTCTTGTCAGCCACTGTTTCGGGAGAGAGTGCTGTCATCAGTTGGTAGAG 979
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Db 980 ATTATCAAGGTTCTTGTTACTCAACCCGCTGAGGAGATAGATGATGATCCCAACTAT 1039
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Db 1040 ACTGAGTTTCAAGTTTCTCAGATAAAGGCTCATCCGTGGCACAAGATTTTCCACAAGAG 1099
Qy 1039 ATGCTCTCCAGAACATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGC 1098
Db 1100 ATGCTCTCCAGAACATAGACCTTGCATCTCGGCTTCTTCAAGTATTCACCAAGTCTTGC 1159
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Db 1160 TGCTCTGCTCTTGACGATCGGCTCATCCCTTCTCGATGAGCTGGGACACCGAACGCA 1219
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Db 1220 CGCTTACCAACGCGCCGCTTCCCTCGCTCTTTAACTTCAAGCAGCAACTAGCAAT 1279
Qy 1219 GCTTCAATGAGCTAATCAACAGGCTAATACCTGAGCATGTGAGAGCAACAAATGAGCACA 1278
Db 1280 GCCTCTCCGACCTCGTACGAGCGCTTGTCGGGAGCACATTAGACGCGATCGGTGTC 1339
Qy 1279 GGATTACAAACAGTTA 1295
Db 1340 AACTCGGGAGCAGCTA 1356

RESULT 6
LOCUS CK266410
DEFINITION EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAC457 5' end, mRNA sequence.
ACCESSION CK266410
VERSION 1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 924)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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source Location/Qualifiers
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/organism="Solanum tuberosum"
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/db_xref="taxon:4113"
/clone="POAC457"
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/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,

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6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match 39.4%; Score 635.4; DB 7; Length 924;
Best Local Similarity 80.8%; Pred. No. 3.3e-154;
Matches 741; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 308 GTTCATTCCGGATTGTTTTCAGGGCAAAATGTTGGAACCTGGAGAACTGAGAGATCAGTAGCCATT 367
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Qy 368 AAAGGCTCTGCAAGTCAGCGCTATAAAACCGTGAGTTGCAACTTAATGCGACCAATGG 427
Db 61 AGAAGGTTTTTACGAGCAAGCGGTATAAAACCGTGAACTACAACCTGATGCGCTTATGG 120
Qy 428 ATCACCCTAAATGTCTATCTCTTGAAGCACTGTTTCTTCTCTACAAAGAGTAGAGATGAGC 487
Db 121 ATCACCCTAAATGTCTATCTTAAAGCACTGCTTCTTCTCCAGCACTAGTAGAGATGAGC 180
Qy 488 TCTTCTCTCAACTGTTTATGAGATATGATACCTGAGACTTTTATACCGGGTTTGGAGCACT 547
Db 181 TTTTCTTAAATTTGGTATGATGATGTCCTTGAAGTTTATACAAGTTTAAAGCACT 240
Qy 548 ATACTAGTTCTAATCAGAGATGCCAAATTTCTATGTCAAGCTTTTACACATATCAATCT 607
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Qy 608 TTAGAGGTTTGGTTTACATCCATCTGTTTCCCGGTGTTTCCACACAGAGATGTGAACCCAC 667
Db 301 TCAGAGGCTGGCTTACATCATATGTTTCCAGAAATTTGCCATAGAGATGTGAACCTC 360
Qy 668 AAAATCTCTGTTGATGATCCCTTGACCCATCAAGTTAAAGTGTGTGATTTTGGAAAGTGCAA 727
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Qy 728 AAGTATTGCTCAAGGTGAACCAACATATATATCTGCTCCCTTATATCGTGCTC 787
Db 421 AAGTCTCTGTTGATGTTGAAGCAAAATTTTCGTACATTTGCTCTCGCTACTACAGAGCTC 480
Qy 788 CAGAACTCATCTTTTGGCGCCACAGAGTATACAGCATCCATAGATATATGTTCTGTGGTT 847
Db 481 CAGAACTCATATTTTGGTGCACAGATATACAACTCAATGATATTTTGTTCAGCAGGCT 540
Qy 848 GTGTACTGCGAGACTTCTTCTTGGCCAGCGTTATTTCCAGAGAGAAATTCAGTTGATC 907
Db 541 GTGTCTCTGCTGAGCTTCTTCTGGGCGAGCGCTCTTCTGCGGCAAAATTCGCGTAGACC 600
Qy 908 AGCTTCTGAGATCATAAAGGTTCTTGGTACTCCCACTGCTGAAGAAATTCGATGTATGA 967
Db 601 AACTGTGTGAGATCATCAAGGTTCTTGGTACTCTTCTACTCGGGAAGAAATTCGATGTATGA 660
Qy 968 ACCCGAACTACACAGATTTTGTAGTTTCCCAAAATCAAGCTCACCTTGGCACAAGTTT 1027
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Qy 1028 TTCAATAAAGGATGCTTCCAGAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTCAC 1087
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Db 781 CAAGTCTTCTGCTGTAAGTCAAGCATGCTGCAATTCATTCCTTGATGAGCTTCGTG 840
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QY 1208 AGTTAGTGGAGCTTCA 1224
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RESULT 7
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LOCUS AV827407 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-15-A20 5',
DEFINITION mRNA sequence.
ACCESSION AV827407
VERSION AV827407.1 GI:19869467
SOURCE EST.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 620)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.,
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Teukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified lambda PLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
FEATURES             Location/Qualifiers
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ORIGIN
Query Match          37.4%; Score 603.4; DB 1; Length 620;
Best Local Similarity 99.2%; Pred. No. 6.7e-146;
Matches 615; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 34 ATTGTTTCAGTGTTCAGAGAGAAAGAGTAAAGACATGCGCTCATTCATTGGGG 93
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Db 1 ATTGTTTCAGTGTTCAGAGAGAAAGAGTAAAGACATGCGCTCATTCATTGGGG 60
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QY 94 CTCAGCTTCATGCTCTTCTCCGCGCTGCGAGCTTCACGAGCGGACGCTTTGAAACGC 153
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Db 61 CCTCAGCCTCATGCTCTTCTCCGCGCTGCGAGCTTCACGAGCGGACGCTTTGAAACGC 120
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Db 121 CGTCTGAATTCGATTCGATAAGGAAATGTTCTCAGCTGTTTATTTAGAGGAAATGACGCT 180
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QY 214 GTTACTGTCATATCATTTCCACTACTATAGAGGCAAAAACGGGCAACCAAGACGAC 273
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Db 181 GTTACTGTCATATCATTTCCACTACTATTTGAGGCAAAAACGGGCAACCAAGACGAC 240
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QY 274 ATTAGTTACATGCGCTGAGCGGTTCTTGGAACAGGTTTCATTCCGGATTGTTTTCAGGGG 333
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DEFINITION Zea mays
ACCESSION AY103545
VERSION AY103545.1 GI:21206623
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1967)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1967)
Coe, E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB, www.zmdb.iastate.edu; TIGR,
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
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Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
Location/Qualifiers
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RESULT 10
LOCUS CL964803
DEFINITION OsIFC011089 Oryza sativa Expressed Sequence Tags (ESTs) from a cDNA library (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION CL964803
VERSION CL964803.1 GI:52384296
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 2295)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
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Matches 711; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

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Qy 486 GCTCTTCTCAACCTGTTTATGAGTATGATCCTGAGACTTTTATACCGGTTTTCAGGCA 545
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846 TTGTGTAGTGGCAGAGCTTCTTGTGGCAGCGGTTATTTCCAGGAGAAAAATTCAGTTGA 905
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CK290108 910 bp mRNA linear EST 02-AUG-2004  
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 end, mRNA sequence.  
 CK290108  
 CK290108.1 GI:39869260  
 EST.  
 Nicotiana benthamiana  
 Nicotiana benthamiana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamids; Solanales; Solanaceae; Nicotiana.  
 1 (bases 1 to 910)  
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
 Staskawicz, B., Jin, H. and Baker, B.  
 Generation of EST sequences from Nicotiana benthamiana  
 Unpublished (2003)  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr, Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 Clones can be requested from the University of Arizona Genomics  
 Institute via http://genome.arizona.edu/orders/  
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 tissues that include callus, roots from liquid culture  
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
 Xanthomonas campestris pv campestris 12 hr, 18hr;  
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
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 these tissues and pooled in approximately equal molar  
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FEATURES

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 tissues that include callus, roots from liquid culture  
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
 Xanthomonas campestris pv campestris 12 hr, 18hr;  
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
 campestris pv vesicatoria 18hr). RNA was isolated from  
 these tissues and pooled in approximately equal molar  
 amounts."

ORIGIN

Query Match 35.6%; Score 575; DB 7; Length 910;  
 Best Local Similarity 77.7%; Pred. No. 1.8e-138;  
 Matches 695; Conservative 0; Mismatches 200; Indels 0; Gaps 0;  
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 Arabidopsis thaliana (thale cress).  
 ACCESSION BX831446

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REFERENCE	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.	Db	744	TACACTTATCAGATCTTAGAGCCTTATCTTACATTTACCGGATGCAATTTGGTGTGTCAT	803
AUTHORS	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation	Qy	652	AGAGATGTGAAACCAACAAATCTCTTGGTGTGATCTCTTGACCCTCAGGTAAAGCTGTCT	711
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AUTHORS	Direct Submission	Qy	772	CGTTATTTATCGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGAT	831
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Db	924	AGTATTATACAGAGCACCTGAACTCATCTTTGGAGCAACCGAGTATACGACAGCCATTGAT	983
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.	Qy	832	ATATGCTCTGCTGGTGTGTAAGTGTGCTGACAGAGCTTCTTTGGCCAGCGTATTATTCAGGA	891
FEATURES	Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length	Db	984	GTCTGGTCTGCAAGGATGTTCTAGCTGAACATTTGCTTGGACAGCCCTTGTTCCTGT	1043
source	http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.	Qy	892	GAAATTCAGTTGATGATCAGCTTGTGGAGATCATATAAGGTTCTTGTGTAATCTCCAACTCGTGAA	951
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AV831097	AV831097	ACCESSION	AV831097	AV831097	
AV831097	AV831097	VERSION	AV831097.1	GI:19873157	
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AV831097	AV831097	SOURCE	Arabidopsis thaliana	Arabidopsis thaliana	
AV831097	AV831097	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
AV831097	AV831097	REFERENCE	1 (bases 1 to 591)	1 (bases 1 to 591)	
AV831097	AV831097	AUTHORS	Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.		



TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: meeki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

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Best Local Similarity 99.2%; Pred. No. 8.9e-138;  
Matches 589; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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RESULT 14  
CB971865  
LOCUS  
DEFINITION CB971865 829 bp mRNA linear EST 30-APR-2003  
CAB10006\_IIIIa\_Fa\_H05 Cabernet Sauvignon Flower Pre-bloom - CAB1  
Vitis vinifera cDNA clone CAB10006\_IIIIa\_Fa\_H05 5', mRNA sequence.

ACCESSION CB971865.1 GI:30255733  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosids; Vitaceae; Vitis.

REFERENCE  
AUTHORS 1 (bases 1 to 829)  
Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J.,  
Jones,K. and Cook,D.  
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'  
berries at various developmental stages  
Unpublished (2003)  
CONTACT: Douglas Cook, PhD  
CAES Genome Facility  
UC Davis, Plant Pathology  
One Shields Ave, Davis, CA 95616, USA  
Tel: 530 754 6561  
Fax: 530 754 6617  
Email: drcook@ucdavis.edu  
Seq primer: ACGGTACCGACATATGCG.

FEATURES  
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vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples  
were collected approximately eleven days before onset of  
bloom (clusters at this stage were fully developed and  
flowers with calyptras or caps still attached. Sampled  
vines were located at the University of California, Davis,  
Experimental Vineyard. cDNAs were made by oligo-dr priming  
and directionally cloned. 5' and 3' adaptors were used in  
cloning as follows:  
5'-ATGCTGTTTTCAGCGGAAATGCTTGGAACTGGAGACTGTGGCCATAAAGGTTCT 376  
5'-ATCTAGAGCGGAGCGGCGGACATG-dT(30)NN-3'. Library was  
constructed using the Clontech Creator SMART kit and  
size-selected to contain the 0.5-3 kb size fraction."

ORIGIN  
Query Match 35.4%; Score 572; DB 6; Length 829;  
Best Local Similarity 80.8%; Pred. No. 1.1e-137;  
Matches 668; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

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Db |||||  
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QY 497 ACCTGTTATGAGTATGACCTGAGACTTTATACCGGTTTTTGAGGCACTATAGTT 556  
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 QY 557 CTAATCAGAGGATGCCAAATTTTCTATGTCAAGCTTTTACACATATCAAAATCTTTAGAGTT 616  
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AY108486 1752 bp mRNA linear HTC 16-OCT-2002  
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ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 1752)  
 Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whiteitt, M.S.,  
 Arthur J.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
 Maize Mapping Project/DuPont Consensus Sequences for Design of  
 Overgo Probes  
 Unpublished (2002)  
 2 (bases 1 to 1752)  
 Coe, E.H.  
 Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, maizenap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.  
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# FEATURES

source

/note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed DuPont contigs; this resource was  
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 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

## ORIGIN

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Db ||||| ||||| |||||
Qy 1300 TTCAATTTTAAGC 1312
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